

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 08:48:08 ; Search time 34.7668 Seconds  
(without alignments)  
913.271 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764

Sequence: 1 ASTKGPVVFPLAPSSKSTSG.....MHEALHNHYQKSLSPGK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARYS

Result No.	Score	Query Match	Length	ID	Description
1	1729	98.0	330	1 GHU	Ig gamma-1 chain C
2	1592.5	90.3	377	2 A23511	Ig gamma-3 chain C
3	1590.5	90.2	377	2 A60764	Ig gamma-3 chain C
4	1566	88.8	326	1 G4HU	Ig gamma-2 chain C
5	1552.5	88.0	327	1 G4HU	Ig gamma-4 chain C
6	1225.5	69.5	374	2 S69339	Ig heavy chain V r
7	1225	69.4	328	2 I47159	Ig gamma 2a chain
8	1222	69.3	355	4 S31866	Ig gamma-1 chain C
9	1219	69.1	328	2 I47160	Ig gamma 2b chain
10	1216	68.9	324	2 PT0207	Ig gamma chain C r
11	1193	67.6	328	2 I47158	Ig gamma 1 chain c
12	1192.5	67.6	323	1 GHRB	Ig gamma chain C r
13	1189	67.4	328	2 I47161	Ig gamma 3 chain c
14	1174.5	66.6	329	1 G2GP	Ig gamma-2 chain C
15	1163.5	66.0	472	2 S31459	Ig gamma-1 chain -
16	1144.5	64.9	470	2 S22080	Ig heavy chain pre
17	1125.5	63.8	308	2 C30554	Ig heavy chain C r
18	1123	63.7	289	1 G3HMI	Ig gamma-3 heavy c
19	1117.5	63.4	333	2 PS0018	Ig gamma-2b chain
20	1116	63.3	444	2 PC4436	monoclonal antibody
21	1114	63.2	326	2 PS0017	Ig gamma-1 chain C
22	1109	62.9	324	1 G1MS	Ig gamma-1 chain C
23	1108	62.8	329	1 G1MSC	Ig gamma-3 chain C
24	1104	62.6	393	1 G1MSM	Ig gamma-1 chain C
25	1097	62.2	398	1 G1MSM	Ig gamma-3 chain C
26	1093	62.0	330	1 G2MSA	Ig gamma-2a chain
27	1093	62.0	469	2 S37483	Ig gamma-2a chain
28	1090.5	61.8	335	1 G2MSAB	Ig gamma-2a chain
29	1088	61.7	399	1 G2MSAM	Ig gamma-2a chain

30	1085.5	61.5	329	2 S00847	Ig gamma-2c chain
31	1078	61.1	446	2 S40295	Ig gamma-2a chain
32	1074	60.9	322	2 PS0019	Ig gamma-2a chain
33	1063.5	60.3	327	2 S06611	Ig gamma-2 chain C
34	1054	59.8	405	1 G2MSBM	Ig gamma-2b chain
35	1039	58.9	475	2 S01321	Ig gamma-2b chain
36	1036.5	58.8	474	1 G2MS11	Ig gamma-2b chain
37	1028	58.3	277	2 I47162	Ig gamma 4 chain C
38	669	37.9	180	2 I46732	Ig epsilon heavy cha
39	648.5	36.8	548	2 S38864	Ig epsilon chain C
40	549	31.1	249	2 S69340	Ig heavy chain VH1
41	547	31.0	218	2 A36040	Ig heavy chain V-I
42	547	31.0	549	2 S04845	Ig heavy chain pre
43	542	30.7	152	2 S14236	Ig gamma-1 chain C
44	534	30.3	220	2 A49444	Ig gamma-1 heavy c
45	532	30.2	241	2 S69131	Ig heavy chain (D0

#### ALIGNMENTS

##### RESULT 1

GHU  
Ig gamma-1 chain C region - human  
C/Species: Homo sapiens (man)  
C/Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #ext change 09-Jul-2004  
C/Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146  
R/Elison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982  
A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.  
A/Reference number: A93433; M0ID:82274238; PMID:6287432  
A/Accession: A93433  
A/Molecule type: DNA  
A/Residues: 1-330 <BL>  
A/Cross-references: UNIPROT:P01857; EMBL:Z17370  
A/Note: This sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) markers, 2 R/Harris, L.J.  
submitted to the EMBL Data Library, October 1992  
A/Reference number: S33904  
A/Accession: S36861  
A/Molecule type: DNA  
A/Residues: 2-330 <HAR>  
A/Cross-references: EMBL:Z17370  
R/Rakhaishi, N.; Ueda, S.; Obata, M.; Nakai, S.; Honjo, T.  
Cell 29, 671-679, 1982  
A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of a  
A/Reference number: S33887; M0ID:83001943; PMID:6811139  
A/Accession: S33887  
A/Molecule type: DNA  
A/Residues: 88-113;235-330 <TAK>  
A/Cross-references: EMBL:Z17370  
R/Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C  
Biochemistry 9, 3161-3170, 1970  
A/Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequenc  
A/Reference number: A90563; M0ID:71064024; PMID:5489771  
A/Contents: myeloma protein Bu  
A/Accession: B90563  
A/Molecule type: protein  
A/Residues: 1-96; 'R', 98-135 <GUN>  
A/Note: this sequence has the Gln(3) marker, 97-Arg  
R/Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970  
A/Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen  
A/Reference number: A90564; M0ID:71064025; PMID:5530842  
A/Contents: Bu  
A/Accession: A90564  
A/Molecule type: protein  
A/Residues: 136-154; 'O', 156-165; 'Q', 167-176; 'O', 178-194; 'N', 196-197; 'D', 199-238; 'E', 240; 'H  
A/Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met  
R/Ponstingl, H.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A/Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nle),



F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 90.2%; Score 1590.5; DB 2; Length 377;

Best Local Similarity 80.1%; Pred. No. 1.1e-102;

Matches 302; Conservative 13; Mismatches 15; Indels 47; Gaps 1;

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QY 1 ASTKPSVFPPLAPSSKSTSGCTAALGCLVKDYFPEPVYTWNMSGALTSGVHPFPAVLQSS 60
DB 1 ASTKPSVFPPLAPSSKSTSGCTAALGCLVKDYFPEPVYTWNMSGALTSGVHPFPAVLQSS 60
QY 61 GLYSLSVTVTVSSSLGDTQYICNVNHPKSNPKVDKVV----- 98
DB 61 GLYSLSVTVTVSSSLGDTQYICNVNHPKSNPKVDKVELKTPGLGDTTHCPRCPEPKSC 120
QY 99 -----EPKSCDKHTHTCPCPAPPELLGSPSVFLFPPPKXDT 133
DB 121 DTRPPCPRCPEPKSCDTPPRCPCPEPKSCDTPPRCPAPPELLGSPSVFLFPPPKXDT 180
QY 124 LMISTRPETCVVVDVSHEDPEVKFNWYVDGVEVHNHVKTKPREEQYNSTYRVSVLTVLH 193
DB 181 LMISTRPETCVVVDVSHEDPEVQFKWYVDGVEVHNHAKTKPREEQYNSTFRVSVLTVLH 240
QY 194 QMMNNGKEKCKVSNKALPAPLEKTSKAKVQPREQVYTLPPSRDELTKNOVSLTCLVK 253
DB 241 QMNLNGKEKCKVSNKALPAPLEKTSKTKGQPREQVYTLPPSRDEMTKNQVSLTCLVK 300
QY 254 GFPPSDIAVEMESNGPENNYKTPPEVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSVME 313
DB 301 GFPPSDIAVEMESSGQPENNYKTPPEVLDSGDFLYSKLTVDKSRWQOGNVFSCSVME 360
QY 314 ALHNHYQQRSLSLSPCK 330
DB 361 ALHNRFQKSLSLSPCK 377
```

#### RESULT 4

G2HU

Ig gamma-2 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text\_change 09-Jul-2004

C:Accession: A93906; A92809; A90752; A93133; A02148

R:Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con

A:Reference number: A93906; MUID:82197621; PMID:6804948

A:Accession: A93906

A:Molecule type: DNA

A:Residues: 1-326 <ELL>

A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; MID:G32759; PIDN:CAB58438.1; F

A>Note: Lys-326 is probably removed posttranslationally

R:Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and E

A:Reference number: A92809; MUID:81007873; PMID:6774012

A:Accession: A92809

A:Molecule type: protein

A:Residues: 1-119, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <MAN>

A>Note: Trp-156 is at or near the complement-binding site

R:Connell, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A:Title: The amino acid sequences of the three heavy chain constant region domains of a

A:Reference number: A90752; MUID:80001357; PMID:113060

A:Accession: A90752

A:Molecule type: protein

A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-

A>Note: this sequence has since been revised

R:Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g

A:Reference number: A93133; MUID:80114419; PMID:118920

A:Contents: Zie

A:Accession: A93132

A:Molecule type: protein

A:Residues: 238-275 <HOF>

R:Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A:Reference number: A94591

A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A>Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic

ned

R:Malstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A:Reference number: A90253; MUID:72033500; PMID:4940472

A:Contents: annotation; myeloma protein Sa, disulfide bonds

R:Frangione, B.; Malstein, C.; Pink, J.R.L.

Nature 221, 145-148, 1969

A:Title: Structural studies of immunoglobulin G.

A:Reference number: A93157; MUID:69064124; PMID:5782707

A:Contents: annotation; Sa, disulfide bonds

C:Genetics:

A:Gene: GDB:IGHG2

A:Cross-references: GDB:119338; OMIM:147110

A:Map position: 14q32.33-14q32.33

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lar

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:133-202/Domain: immunoglobulin homology <IM2>

F:239-306/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83,140-200,246-304/Disulfide bonds: #status experimental

F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.8%; Score 1566; DB 1; Length 326;

Best Local Similarity 89.1%; Pred. No. 4.4e-101;

Matches 294; Conservative 15; Mismatches 17; Indels 4; Gaps 2;

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QY 1 ASTKPSVFPPLAPSSKSTSGCTAALGCLVKDYFPEPVYTWNMSGALTSGVHPFPAVLQSS 60
DB 1 ASTKPSVFPPLAPSSKSTSGCTAALGCLVKDYFPEPVYTWNMSGALTSGVHPFPAVLQSS 60
QY 61 GLYSLSVTVTVSSSLGDTQYICNVNHPKSNPKVDKVKPKSCDKHTHTCPCPAPPELLG 120
DB 61 GLYSLSVTVTVSSSLGDTQYICNVNHPKSNPKVDKVKPKSCDKHTHTCPCPAPPELLG 120
QY 121 PSVFLFPPPKXDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNHVKTKPREEQYN 180
DB 117 PSVFLFPPPKXDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNHAKTKPREEQFN 176
QY 181 STYRVSVTVTVHOMWNGKEKCKVSNKALPAPLEKTSKAKVQPREQVYTLPPSRDE 240
DB 177 STYRVSVTVTVHOMWNGKEKCKVSNKALPAPLEKTSKTKGQPREQVYTLPPSRDE 236
QY 241 LTRKQVSLTCLVKGFFPSDIAVEMESNGPENNYKTPPEVLDSVGSFFLYSKLTVDKSRW 300
DB 237 LTRKQVSLTCLVKGFFPSDIAVEMESNGPENNYKTPPEVLDSGDFLYSKLTVDKSRW 296
QY 301 QOGNVFSCSVMEALHNHYQQRSLSLSPCK 330
DB 297 QOGNVFSCSVMEALHNHYQKSLSLSPCK 326
```

#### RESULT 5

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 02-Apr-1982 #sequence revision 02-Apr-1992 #text\_change 09-Jul-2004

C:Accession: A90933; A80249; A02150

R:Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; UID:83157104; PMID:6299662  
A:Accession: A90933  
A:Molecule type: DNA  
A:Residues: 1-327 <EL>  
A:Cross-references: UNIPROT:P01861  
A>Note: the sequence was determined from the germline gene  
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Mistein, C.  
Biochem. J. 117, 33-47, 1970  
A>Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant r  
A:Reference number: A90249; UID:70207560; PMID:4192699  
A:Accession: A90249  
A:Molecule type: protein  
A:Residues: 1-30;81-326 <PIN>  
C:Genetics:  
A:Gene: GDB:IGHG4  
A:Cross-references: GDB:119340; OMIM:147130  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1, 111/1, 221/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:99-110/Region: hinge  
F:134-203/Domain: immunoglobulin homology <IM2>  
F:240-307/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83, 141-201, 247-305/Disulfide bonds: #status predicted  
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:177/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 88.0%; Score 1552.5; DB 1; Length 327;  
Best Local Similarity 88.8%; Pred. No. 3.8e-100;  
Matches 293; Conservative 15; Mismatches 19; Indels 3; Gaps 1;

QY 1 ASTGSPVPLAPSSKSTSGTAAAGCLVKDYFPPPVTVSNNSGALTSGVHTFPAVLQSS 60  
DB 1 ASTGSPVPLAPSSKSTSGTAAAGCLVKDYFPPPVTVSNNSGALTSGVHTFPAVLQSS 60  
QY 61 GLYSLSVTVVSSSLGTYICNNVHKPSNPKVDKVPKSCDKHTPCPPAPPELLGG 120  
DB 61 GLYSLSVTVVSSSLGTYICNNVHKPSNPKVDKVPKSCDKHTPCPPAPPELLGG 117  
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180  
DB 118 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 177  
QY 181 SYRVSVALTVLHOMMNGEKYCKVKSNKALPAPKEKTSKAKVQPREPOVYTLPPSRDE 240  
DB 178 SYRVSVALTVLHOMMNGEKYCKVKSNKALPAPKEKTSKAKVQPREPOVYTLPPSRDE 237  
QY 241 LTKQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDVSGSFLLYSKLTVDKSRM 300  
DB 238 MTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDVSGSFLLYSKLTVDKSRM 297  
QY 301 QGQNVFSCSVMEALHNNYQKRSLSLSPGK 330  
DB 298 QGQNVFSCSVMEALHNNYQKRSLSLSPGK 327

RESULT 6  
S69339  
Ig heavy chain V region precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #ext\_change 01-Dec-2000  
C:Accession: S69339; S72664  
R:Khamilich, A.A.; Auncuturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A>Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; UID:95262687; PMID:7744049  
A:Accession: S69339  
A:Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-374 <KHA>  
A:Cross-references: EMBL:X81695  
R:Khamilich, A.A.  
submitted to the EMBL Data Library, September 1994  
A:Reference number: S72664  
A:Accession: S72664  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140, C', 142-374 <KH2>  
A:Cross-references: EMBL:X81695  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 69.5%; Score 1225.5; DB 2; Length 374;  
Best Local Similarity 87.1%; Pred. No. 1.8e-77;  
Matches 230; Conservative 6; Mismatches 17; Indels 11; Gaps 2;

QY 78 TQTYICNNV-----HK-PSNTKYDKKPKSCDKHTPCPPAPPELLGSPVFLF 126  
DB 111 TATYICGYSVEGGYGRFHSKGGTTLTVSSEPKCKHTPCPPAPPELLGSPVFLF 170  
QY 127 PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTRYV 186  
DB 171 PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTRYV 230  
QY 187 SVLTVLHOMMNGEKYCKVKSNKALPAPKEKTSKAKVQPREPOVYTLPPSRDELTKNOV 246  
DB 231 SVLTVLHOMMNGEKYCKVKSNKALPAPKEKTSKAKVQPREPOVYTLPPSRDELTKNOV 290  
QY 247 SLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDVSGSFLLYSKLTVDKSRMQQGVNF 306  
DB 291 SLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDVSGSFLLYSKLTVDKSRMQQGVNF 350  
QY 307 SCSVMHEALHNNYQKRSLSLSPGK 330  
DB 351 SCSVMHEALHNNYQKRSLSLSPGK 374

RESULT 7  
I47159  
Ig gamma 2a chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #ext\_change 21-Jan-2000  
C:Accession: I47159  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A>Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s  
A:Reference number: I47159; UID:95015845; PMID:7930579  
A:Accession: I47159  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03779; NID:g433123; PID:AAA52217.1; PID:g433124  
C:Genetics:  
A:Gene: IGG2a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IM4>

Query Match 69.4%; Score 1225; DB 2; Length 328;  
Best Local Similarity 67.5%; Pred. No. 1.7e-77;  
Matches 224; Conservative 46; Mismatches 56; Indels 6; Gaps 2;

QY 1 ASTGSPVPLAPSSKSTSGTAAAGCLVKDYFPPPVTVSNNSGALTSGVHTFPAVLQSS 60  
DB 1 AKPTAPSVPLAPCSRDTSGPNVALGLASSYFPPPVTVSNNSGALTSGVHTFPAVLQSS 60  
QY 61 GLYSLSVTVVSSSLGTYICNNVHKPSNPKVDKVPKSCDKHTPCPPAPPELLGG 120  
DB 61 GLYSLSVTVVSSSLGTYICNNVHKPSNPKVDKVPKSCDKHTPCPPAPPELLGG 116  
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180  
DB 117 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 176



QY 181 STYRVSVTLVHQNMMNGEKCKVSNKALPAPIKTISSKAKVQPREPOVYTLPPSRDE 240  
Db 177 STYRVSVTLPIQHODMLNKEKCKVNNKDLPAPIRIIISKAKGQTRPEQVYTLPPHAE 236  
QY 241 LTKNOVSLTCLVKGFYPSDIAVEMESNGO--PENNYKTTTPVLDVSGSFYLSKLTVDKS 298  
Db 237 LSRKSVITCLVIGFYPPIDVEMQNGQPREPGNRTTPPOODVDGTFFLYSKFSVDKA 296  
QY 299 RWQGNVFSQSVMEALHNHYOQRSLSLSPGK 330  
Db 297 SWGGGIFQCVAWHEALHNHYQKSIKTPGK 328

## RESULT 8

Ig gamma-1 chain C region - synthetic

C/Species: synthetic  
A/Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C/Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C/Accession: S31866  
R.Filipula, D.  
submitted to the EMBL Data Library, February 1993  
A/Description: Screening method for protein-protein interactions of cloned gene products.  
A/Reference number: S31866  
A/Accession: S31866  
A/Molecule type: mRNA  
A/Residues: 1-255 <FIL>  
A/Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49666.1; PID:g33069  
C/Keywords: immunoglobulin  
F.1-22/Region: Escherichia coli outer membrane protein A precursor  
F.23-255/Region: human Ig gamma-1 chain C region

Query Match 69.3%; Score 1222; DB 4; Length 255;  
Best Local Similarity 94.6%; Pred. No. 2e-77;

Matches 226; Conservative 3; Mismatches 10; Indels 0; Gaps 0;  
QY 92 TVDKKVEKSCDKHTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSH 151  
Db 17 TVAQADVESKSCDKHTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSH 76  
QY 152 EDPVEKFNMYVDGVEVHNKTKPREQYNSTRVSVTLVHQNMMNGEKCKVSNKAL 211  
Db 77 EDPVEKFNMYVDGVEVHNKTKPREQYNSTRVSVTLVHQNMMNGEKCKVSNKAL 136  
QY 212 PAPIKTISSKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPE 271  
Db 137 PAPIKTISSKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPE 196  
QY 272 NNYKTTTPVLDVSGSFYLSKLTVDKSRWQGNVFSQSVMEALHNHYOQRSLSLSPGK 330  
Db 197 NNYKTTTPVLDVSGSFYLSKLTVDKSRWQGNVFSQSVMEALHNHYOQRSLSLSPGK 255

## RESULT 9

Ig gamma 2b chain constant region - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C/Accession: I47160  
R.Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A/Reference number: I47158; NUID:95015845; PMID:7930579  
A/Accession: I47160  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-328 <KAC>  
A/Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126  
C/Genetics:  
A/Gene: IGG2b  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
F.133-202/Domain: immunoglobulin homology <IGM>

Query Match 69.1%; Score 1219; DB 2; Length 328;  
Best Local Similarity 67.2%; Pred. No. 4.3e-77;  
Matches 223; Conservative 45; Mismatches 58; Indels 6; Gaps 2;

QY 1 ASTKGSVPLPAPSSKSTSGTAAGCLVKDYFPPEPVTSNMSGALTSQVHFPATQSS 60  
Db 1 APTKALVPLPAPCGSDTSGPNVALGCLASSTPPEPVYTNMSGALTSQVHFPATQSS 60  
QY 61 GLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVRPKSCDKHTHTCPCPAPPELLG 120  
Db 61 GLYSLSMTVTVASSLSSSYTCNNVHRPATTTKVDKVRGCTKTRPPDICAPESP-----G 116  
QY 121 PSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNKTKPREQYN 180  
Db 117 PSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNKTKPREQYN 176  
QY 181 STYRVSVTLVHQNMMNGEKCKVSNKALPAPIKTISSKAKVQPREPOVYTLPPSRDE 240  
Db 177 STYRVSVTLPIQHODMLNKEKCKVNNKDLPAPIRIIISKAKGQTRPEQVYTLPPHAE 236  
QY 241 LTKNOVSLTCLVKGFYPSDIAVEMESNGO--PENNYKTTTPVLDVSGSFYLSKLTVDKS 298  
Db 237 LSRKSVITCLVIGFYPPIDVEMQNGQPREPGNRTTPPOODVDGTFFLYSKFSVDKA 296  
QY 299 RWQGNVFSQSVMEALHNHYOQRSLSLSPGK 330  
Db 297 SWGGGIFQCVAWHEALHNHYQKSIKTPGK 328

## RESULT 10

Ig gamma chain C region - chimpanzee

C/Species: Pan troglodytes (chimpanzee)  
C/Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 16-Jul-1999  
C/Accession: PT0207  
R.Shirich, P.H.; Moustafa, Z.A.; Oestberg, L.  
Mol. Immunol. 28, 319-322, 1991  
A/Title: Nucleotide sequence of chimpanzee Fc and hinge regions.  
A/Reference number: PT0207; NUID:91287716; PMID:2062315  
A/Accession: PT0207  
A/Molecule type: mRNA  
A/Residues: 1-234 <EHR>  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F.48-117/Domain: immunoglobulin homology <IGM>

Query Match 68.9%; Score 1216; DB 2; Length 234;  
Best Local Similarity 95.7%; Pred. No. 4.6e-77;

Matches 224; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 90 SNTKVDKVEKSCDKHTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDV 149  
Db 1 SNTKVDKVEKSCDKHTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDV 60  
QY 150 SHEDPEVKFNMYVDGVEVHNKTKPREQYNSTRVSVTLVHQNMMNGEKCKVSNK 209  
Db 61 SHEDPEVKFNMYVDGVEVHNKTKPREQYNSTRVSVTLVHQNMMNGEKCKVSNK 120  
QY 210 ALPAPIKTISSKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGO 269  
Db 121 ALPAPIKTISSKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGO 180  
QY 270 PENNYKTTTPVLDVSGSFYLSKLTVDKSRWQGNVFSQSVMEALHNHYOQRSLSLSPGK 323  
Db 181 PENNYKTTTPVLDVSGSFYLSKLTVDKSRWQGNVFSQSVMEALHNHYOQRSLSLSPGK 234

## RESULT 11

I47158

Ig gamma 1 chain constant region - pig (fragment)  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C/Accession: I47158



Query Match	67.4%	Score 1189	DB 2	Length 328
Best Local Similarity	66.9%	Pred. No. 5.1e-75		
Matches 222	Conservative 43	Mismatches 61	Indels 6	Gaps 3
Qy	1	ASTKGPVFPPLAASSKSTSGTALGCLVWKYFPPEPVTSWNSGALTSVHTFPFAVLQSS	60	
Db	1	APKTAPEVYPLAPCGRDTSGPNVALGCLASFPPEPVMTNNSGALTSVHTFPFSVLQPS	60	
Qy	61	GLYSLSVVTVPPSSSLGTQYICVNNHKPSNTKYDKKYEPKSCDKHTTCPPCAPELLGG	120	
Db	61	GLYSLSMTVTVPASSLSKSKSYTCNNVHPATTTKDKKDVGTKT--KPPCIPCPCCE-VAG	116	
Qy	121	PSVFLFPFKPKDITLMSRTPEVTCVVVDVSHEDPEVKPMWVDVDEVHNVKTRKEEQYN	180	
Db	117	PSVFIFPPKPKDITLMSQTPEVTCVVVDVSHEDPEVKPMWVDVDEVHNVKTRKEDEQFN	176	
Qy	181	STRVAVSVLTIVLHONNMNMGKEKCKVSNKALPAIEIKTISKAKQPREPQVYTLPPSRDE	240	
Db	177	STRVAVSVLPIQHODMLKGEFKCKKANNVNDLPALITRTISALIQSNRPQVYTLPPRAEE	236	
Qy	241	LTKNQVSLTCLVKGFYPSDIAAVEMESNQ--PENNYKTTPEPVLDVSQGSFYLSTLVYDKS	298	
Db	237	LSRSKVTIVTCIVGIFYPPDIIHVEKWSNQGPPEGNYRTTPQOQVDGTFFLYSKLADVKA	296	
Qy	299	RMQGNVFPSCSVMEALHNHYQQRSLSPSK	330	
Db	297	RMDSGETPECAVMEALHNHYTKSISTKQK	328	

**RESULT 14**  
**G2GP**

A:Reference number: A90354; MUID:71058474; PMID:4922544  
A:Contents: annotation; disulfide bonds  
A>Note: Cys-16 is involved in a heavy-light chain bond  
A>Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds  
C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as Iga and Igi, the subunits associate into larger chain disulfide bonds.  
C:Superfamily: immunoglobulin C region, immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
E:21-81/Domain: immunoglobulin homology <IM1>  
E:135-204/Domain: immunoglobulin homology <IM2>  
E:241-310/Domain: immunoglobulin homology <IM3>  
E:28-79/Disulfide bonds: #status experimental  
E:142-202/Disulfide bonds: #status experimental  
E:178/Binding site: carbohydrate (asn) (covalent) #status experimental  
E:248-308/Disulfide bonds: #status experimental

Query Match	Similarity	66.6%	Score 1174.5	DB 1	Length 329
Best Local	Similarity	68.2%	Pred. No. 5.2e-74		
Matches	Conservative	31	Mismatches 66	Indels 9	Gaps 4
Qy	1	ASTKGPVSFPAPASKSTSGTAAAGCVCWKDYFPEPVYVSNMGSALITSGVHTPEAVLQSS	60		
Db	2	ARTAPSVFPLAASGVDTSSGMWMLTGLCYKGFPEPVLYKMGSGALLTSVHTFPALQ-S	60		
Qy	61	GLYSLISVTVVPSSSLGTQTYI CNVNHKPSNTKVDKVKPEKSCDKTH--TCPPCAPELL	118		
Db	61	GLYSLTSMVTVPPSSQKAT-----CNVAHPASSTKVDKTEVPIRTPPBPCTCKCPPEPNI	116		
Qy	119	GGSPVFLPFPKPKDTLMSRTPEVVCVVVDYHEDPEVKFNNYVGVCHNNTKTRREQ	178		
Db	117	GGSPVFIFPPKPKDTLMSLTPEVTCVVVDYSDDEPEVQFTWFDNKPVGNAETKRVED	176		
Qy	179	YNSYTRVVSVLTVLHQNMMNGEKYKCKYSNKALPAPIEKTISKAKVQPREPOVYTLPPSR	238		
Db	177	YNTIFRVVSVPFIQHQDMLRGKEFKCKYKNALPAPIETIKTISKTGAPRMPDYTLPPSR	236		
Qy	239	DELTKNOVSLTCLVKGFPYPSDIJAVWESNGQP--ENNYKTPPVLDSVGSFPLYSKLTVD	296		
Db	237	DELSKISKSVTCLLIINFPADIIHWEASNNRPVVSSEKYEKNTPEPDIADGDSFLYSKLTVD	296		
Qy	297	KSRWQGGVNFSCSVNHEALNHNHYOORSLISLSPG	329		
Db	297	KSAMDQGVTVTCSVNHEALNHNVTOKALSRSPG	329		

RESULT 15  
S31459  
Ig gamma-1 chain - sheep (fragment)  
C|Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C|Date: 13-Jan-1995 #sequence\_13-Jan-1995 #text\_change 16-Jul-1999  
C|Accession: S31459  
R|Patri, S.; Nau, F.  
submitted to the EMBL Data Library, December 1992  
A|Reference number: S31459  
A|Accession: S31459  
A|Status: preliminary  
A|Molecule type: mRNA  
A|Residues: 1-472 <PAT>  
A|Cross-references: EMBL:X69797  
C|Superfamily: immunoglobulin C region; immunoglobulin homology  
C|Keywords: immunoglobulin  
;1277-346/Domain:immunoglobulin homology <IMM>

[illegible]

Db 202 GUYSSSVTVTPASTSGAOTFICNVAHPASSTKVDKRVEPGCPDPECKHC-RCPPBELPBG 260  
Qy 121 PSVFLFPPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNNVYDGEVHNVTKTTPREBOYN 180  
Db 261 PSVFLFPPKPKDITLISGTPEVTCVVVDVGDDPEVQFSMFVDNVEVRRARTKPREBOFN 320  
Qy 181 STYRVVSVLTUHQWMNGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240  
Db 321 STFRVVSALPIQHODMTGKEFKCKVHNALPAPIVRTISRTKGQAREPOVYVLAPOEE 380  
Qy 241 LTKNOVSLTCLVKGFYPSDIAVEMESNGOP--ENNYKTTPVLDISVGSFELYSKLTVDKS 298  
Db 381 LSKSTLSVTCLVTFYPDYIAVEMQKNQGPESSEDKYGITTSQLDADGSTFLYSRLRVDKN 440  
Qy 299 RWQGNVFSQSVMHENLHNHYOQRSLSLSPGK 330  
Db 441 SWQEGDYACVVMHEALHNHYTQKSISKPPGK 472

Search completed: June 7, 2005, 09:02:33  
Job time : 35.7668 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: June 7, 2005, 08:39:41 ; Search time 162.435 Seconds  
(without alignments)  
1040.329 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764  
Sequence: 1 ASTKGPSVFPAPSSKSTSG.....MHEALHNHYQSRSLSPGK 330

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1729	98.0	330	1 GCI_HUMAN	P01857 homo sapien
2	1729	98.0	465	2 O6GMX6	O6GMX6 homo sapien
3	1729	98.0	469	2 O7ZRP5	O7ZRP5 homo sapien
4	1729	98.0	470	2 O6RJA4	O6RJA4 homo sapien
5	1729	98.0	470	2 O7ZSW1	O7ZSW1 homo sapien
6	1729	98.0	475	2 O6GMW7	O6GMW7 homo sapien
7	1729	98.0	476	2 O6GMX1	O6GMX1 homo sapien
8	1726	97.8	466	2 O6IN78	O6IN78 homo sapien
9	1726	97.8	472	2 O6N089	O6N089 homo sapien
10	1725	97.8	473	2 O6P055	O6P055 homo sapien
11	1725	97.8	475	2 O6MZQ6	O6MZQ6 homo sapien
12	1725	97.8	480	2 O6N094	O6N094 homo sapien
13	1725	97.8	481	2 O6N097	O6N097 homo sapien
14	1725	97.8	482	2 O7Z351	O7Z351 homo sapien
15	1722	97.6	466	2 O6N096	O6N096 homo sapien
16	1720	97.5	348	2 O6PYX1	O6PYX1 homo sapien
17	1720	97.5	478	2 O6P181	O6P181 homo sapien
18	1720	97.5	480	2 O6RUF1	O6RUF1 homo sapien
19	1718	97.4	475	2 O6N095	O6N095 homo sapien
20	1718	97.4	544	2 O6RUV5	O6RUV5 homo sapien
21	1710	96.9	473	2 O6MZV7	O6MZV7 homo sapien
22	1592.5	90.3	518	2 O6N030	O6N030 homo sapien
23	1588.5	90.1	521	2 O8N4Y9	O8N4Y9 homo sapien
24	1577.5	89.4	509	2 O8N4Y9	O8N4Y9 homo sapien
25	1566	88.8	326	1 GC2_HUMAN	P01859 homo sapien
26	1566	88.8	417	2 O6N093	O6N093 homo sapien
27	1561	88.5	465	2 O6P0C4	O6P0C4 homo sapien
28	1552.5	88.0	327	1 GC4_HUMAN	P01861 homo sapien
29	1552.5	88.0	473	2 O8TC63	O8TC63 homo sapien
30	1552	88.0	493	2 O6RNC4	O6RNC4 homo sapien
31	1551	87.9	464	2 O6MZU6	O6MZU6 homo sapien

32	1543.5	87.5	476	2 O6MZX7	O6MZX7 homo sapien
33	1486.5	84.3	354	2 O8ET2	O8ET2 homo sapien
34	1228.5	69.6	337	2 O95M34	O95M34 equus caball
35	1226	69.5	679	2 O96PQ8	O96PQ8 homo sapien
36	1210.5	68.6	487	2 O65ZL2	O65ZL2 mus sp. fcv/
37	1192.5	67.6	323	1 GC_RABIT	P01870 oryctolagus
38	1174.5	66.6	329	1 GC2_CAVPO	P01862 cavia porce
39	1128	63.9	290	1 GC3_HUMAN	P01860 homo sapien
40	1117.5	63.4	333	1 GCB_RAT	P20761 rattus norv
41	1117	63.3	463	2 O99LC4	O99LC4 mus musculu
42	1116	63.3	458	2 O65Z01	O65Z01 homo sapien
43	1114	63.2	326	2 GC1_RAT	P20759 rattus norv
44	1110	62.9	470	2 Q7TMK1	Q7TMK1 mus musculu
45	1109	62.9	324	1 GCI_MOUSE	P01868 mus musculu

## ALIGNMENTS

RESULT 1  
ID GCI\_HUMAN STANDARD; PRT; 330 AA.  
AC P01857;  
DT 21-JUL-1986 (rel. 01, Created)  
DT 21-JUL-1986 (rel. 01, Last sequence update)  
DT 25-OCT-2004 (rel. 45, Last annotation update)  
DE IG gamma-1 chain C region.  
GN Name-IGHG1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82274238; PubMed=6287432;  
RA Ellison J.W., Berson B.D., Hood L.B.;  
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";  
RL Nucleic Acids Res. 10:4071-4079(1982).  
RN [2]  
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).  
RX MEDLINE=71064024; PubMed=5489771;  
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
Waxdal M.J., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
RN Biochemistry 9:3161-3170(1970).  
RN [3]  
RP SEQUENCE OF 136-329 (EU).  
RX MEDLINE=71064025; PubMed=5530842;  
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,  
Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";  
RN Biochemistry 9:3171-3181(1970).  
RN [4]  
RP SEQUENCE (MYELOMA PROTEIN NIE).  
RX MEDLINE=77070269; PubMed=826475;  
RA Ponstingl H., Hilschmann N.;  
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein N1e). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and RT discussion of the complete structure.";  
RN Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
RN [5]  
RP SEQUENCE (MYELOMA PROTEIN KOL) AND DISULFIDE BONDS.  
RX MEDLINE=83289131; PubMed=6884994;  
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
RN Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
RN [6]  
RP DISULFIDE BONDS.  
RX MEDLINE=71064027; PubMed=4923144;

RA Gail W.E., Edelman G.M.:  
RT "The covalent structure of a human gamma G-immunoglobulin. X.  
RL Intrachain disulfide bonds."  
RN Biochemistry 9:3188-3196(1970).  
RX [7]  
RP DISULFIDE BONDS.  
RX MEDLINE=77070267; PubMed=1002129;  
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.:  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein N1e), i: purification and  
RT characterization of the protein, the L- and H-chains, the cyanogen  
RT bromide cleavage products, and the disulfide bridges."  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
RP [8]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE=81208100; PubMed=7236608;  
RA Deisenhofer J.:  
RT "Crystallographic refinement and atomic models of a human Fc fragment  
RT and its complex with fragment B of protein A from Staphylococcus  
RT aureus at 2.9- and 2.8-A resolution."  
RN Biochemistry 20:2361-2370(1981).  
CC -1- MISCELLANEOUS: N1e has the G1M(17) allotypic marker, 97-K, and the  
CC G1M(1) marker, 239-D and 241-L. KOL and EU sequences have the  
CC G1M(3) marker and the G1M (non-1) markers.  
CC -1- MISCELLANEOUS: N1e also differs in the amidation states of 35,  
CC 116, 198, 269 and 272.  
CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues  
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
CC 268-272.  
CC -1- MISCELLANEOUS: KOL also differs in the amidation states of  
CC residues 198, 267 and 272.  
-----  
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-----  
CC EMBL; J00228; AAC82527.1; ALT\_INIT.  
CC PIR; A93433; GHU.  
DR PDB; 1A77; X-ray; H=1-103.  
DR PDB; 1D5B; X-ray; B/H=1-101.  
DR PDB; 1D5I; X-ray; H=1-101.  
DR PDB; 1DN2; X-ray; A/B=120-326.  
DR PDB; 1E4K; X-ray; A/B=106-329.  
DR PDB; 1FC1; X-ray; A/B=106-329.  
DR PDB; 1FC2; X-ray; D=106-329.  
DR PDB; 1FC3; X-ray; A=121-326.  
DR PDB; 1H2H; X-ray; H/K=1-330.  
DR PDB; 1I7Z; X-ray; B/D=1-103.  
DR PDB; 1IIS; X-ray; A/B=107-330.  
DR PDB; 1IIX; X-ray; A/B=107-330.  
DR PDB; 1I6X; X-ray; A=120-326.  
DR PDB; 1QOX; X-ray; A/B=119-350.  
DR PDB; 2RCS; X-ray; H=1-103.  
DR GeneW; HGNC:5525; IGHG1.  
DR MIM: 147100; -.  
DR GO; GO:0005624; C:membrane fraction; NAS.  
DR GO; GO:0003823; P:antigen binding; TAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; Ig\_3.  
DR PROSITE; PS50835; IG\_LIKE; 3.  
DR PROSITE; PS50290; IG\_MHC; 2.  
KW 3D-structure; Direct protein sequencing; Glycoprotein;  
KW Immunoglobulin C region; Immunoglobulin domain.  
FT NON TER 1 98 CH1.  
FT DOMAIN 1 98 CH1.  
FT DOMAIN 99 110 Hinge.

FT	DOMAIN	111	223	CH2.
FT	DOMAIN	224	330	CH3.
FT	DISULFID	27	83	Interchain (with light chain).
FT	DISULFID	103	103	Interchain (with heavy chain).
FT	DISULFID	109	109	Interchain (with heavy chain).
FT	DISULFID	112	112	Interchain (with heavy chain).
FT	DISULFID	144	204	
FT	DISULFID	250	308	
FT	CARBOHYD	180	180	
FT	VARIANT	97	97	
FT	VARIANT	239	239	
FT	VARIANT	241	241	
FT	STRAND	23	24	
FT	STRAND	26	33	
FT	STRAND	38	38	
FT	STRAND	41	41	
FT	TURN	42	45	
FT	TURN	48	49	
FT	STRAND	50	52	
FT	STRAND	57	58	
FT	TURN	59	61	
FT	STRAND	62	71	
FT	HELIX	73	75	
FT	TURN	76	78	
FT	STRAND	82	87	
FT	TURN	88	91	
FT	STRAND	92	97	
FT	TURN	102	103	
FT	STRAND	122	126	
FT	HELIX	130	134	
FT	TURN	136	137	
FT	STRAND	141	149	
FT	STRAND	157	162	
FT	TURN	163	164	
FT	STRAND	165	167	
FT	STRAND	171	172	
FT	STRAND	176	177	
FT	TURN	179	180	
FT	STRAND	183	190	
FT	HELIX	193	197	
FT	TURN	198	199	
FT	STRAND	202	207	
FT	TURN	209	210	
FT	STRAND	215	219	
FT	STRAND	227	227	
FT	STRAND	230	234	
FT	HELIX	238	242	
FT	STRAND	245	256	
FT	TURN	261	266	
FT	TURN	267	268	
FT	STRAND	269	270	
FT	STRAND	274	276	
FT	STRAND	280	281	
FT	TURN	283	284	
FT	STRAND	287	296	
FT	HELIX	297	301	
FT	TURN	302	303	
FT	STRAND	306	311	
FT	TURN	313	314	
FT	HELIX	316	318	
FT	STRAND	319	324	
SQ	SEQUENCE	330 AA;	36106 MW;	3770EE106C2FA3D CRC64;

Query Match 98.0%; Score 1729; DB 1; Length 330;  
Best Local Similarity 97.9%; Pred. No. 3e-118;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY	1	ASTKGPVFPPLAPSSKSTSGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLOSS	60
DB	1	ASTKGPVFPPLAPSSKSTSGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLOSS	60



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QY 61 GLYSLSVVTVVPSSSLGTQTYI CNVNHKPSNTKVDKVEPKSCDTHHTCPCPAPABELLGG 120
DB 61 GLYSLSVVTVVPSSSLGTQTYI CNVNHKPSNTKVDKVEPKSCDTHHTCPCPAPABELLGG 120
QY 121 PSVFLFPPPKDPTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAVKTKRPREEOYN 180
DB 121 PSVFLFPPPKDPTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAVKTKRPREEOYN 180
QY 181 STYRVSVLTVLHQWMNKGKEYCKCKVSNKALPAPIEKITSKAKVQPREPOVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQWMNKGKEYCKCKVSNKALPAPIEKITSKAKVQPREPOVYTLPPSRDE 240
QY 241 LTKNOVSLTCLVKGFPSPDIAVWESNQGPNENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
DB 241 LTKNOVSLTCLVKGFPSPDIAVWESNQGPNENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
QY 301 OQGNVFCSCVMHEALHNHYQKSLSPCK 330
DB 301 OQGNVFCSCVMHEALHNHYQKSLSPCK 330

RESULT 2
Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC 05-JUL-2004 (TREMBLrel. 27, Created)
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Struhsberg R.;
DB Submitted (JUN-2004) to the EMBL/GenBank/DDB databases.
DR EMBL, BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF0047; Ig_4.
DR Pfam; PF00409; Ig_2.
DR SMART; SM00407; IgC1; 3.
```

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DR SMART, SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 465 AA; 51063 MW; B3A9B7D0FD13866 CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 465;
Best Local Similarity 97.9%; Pred. No. 4,5e-116;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKPSVPLAPSSKSTSGGTAALGCVKDYFEPVTVSNWNGALTSVHFPAVLQSS 60
DB 136 ASTKPSVPLAPSSKSTSGGTAALGCVKDYFEPVTVSNWNGALTSVHFPAVLQSS 195
QY 61 GLYSLSVVTVVPSSSLGTQTYI CNVNHKPSNTKVDKVEPKSCDTHHTCPCPAPABELLGG 120
DB 196 GLYSLSVVTVVPSSSLGTQTYI CNVNHKPSNTKVDKVEPKSCDTHHTCPCPAPABELLGG 255
QY 121 PSVFLFPPPKDPTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAVKTKRPREEOYN 180
DB 256 PSVFLFPPPKDPTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAVKTKRPREEOYN 315
QY 181 STYRVSVLTVLHQWMNKGKEYCKCKVSNKALPAPIEKITSKAKVQPREPOVYTLPPSRDE 240
DB 316 STYRVSVLTVLHQWMNKGKEYCKCKVSNKALPAPIEKITSKAKVQPREPOVYTLPPSRDE 375
QY 241 LTKNOVSLTCLVKGFPSPDIAVWESNQGPNENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
DB 376 LTKNOVSLTCLVKGFPSPDIAVWESNQGPNENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 435
QY 301 OQGNVFCSCVMHEALHNHYQKSLSPCK 330
DB 436 OQGNVFCSCVMHEALHNHYQKSLSPCK 465

RESULT 3
Q727P5 PRELIMINARY; PRT; 469 AA.
AC Q727P5;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE IGHG1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
```

RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC051328; AAH51328.1; -  
 DR HSSP; P01857; 1HZH.  
 DR InterPro; IPR007110; IG-1-like.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF07654; C1-set; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 469;  
 Best Local Similarity 97.9%; Pred. No. 4,5e-118;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

DB 1 ASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNGALTSGVHTFPAVLQSS 60  
 140 ASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNGALTSGVHTFPAVLQSS 199

QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHRKSNLKVKPKESCDTHRCPCPAPPELLGG 120  
 200 GLYSLSVVTVPSSSLGTQTYICNVNHRKSNLKVKPKESCDTHRCPCPAPPELLGG 259

QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAVKTKRPREQYN 180  
 260 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAVKTKRPREQYN 319

DB 181 STYRVSVTLTVLHQWMNNGEKYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 240  
 320 STYRVSVTLTVLHQWMNNGEKYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 379

QY 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSGVSFFLYSKLTVDKSRW 300  
 380 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSGVSFFLYSKLTVDKSRW 439

DB 301 QOQNVFSCSVMEALHNHYQOQSLSLSPGK 330  
 440 QOQNVFSCSVMEALHNHYQOQSLSLSPGK 469

QY 440 QOQNVFSCSVMEALHNHYQOQSLSLSPGK 469

RESULT 4  
 Q6PJA4 PRELIMINARY; PRT; 470 AA.

AC Q6PJA4;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 NCBI\_TaxID=9606;  
 RX NCBI\_TaxID=9606;  
 RA SEQUENCE FROM N.A.  
 RP TISSUE=Primary B-Cells;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.;  
 RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC051328; AAH51328.1; -  
 DR HSSP; P01857; 1HZH.  
 DR InterPro; IPR007110; IG-1-like.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF07654; C1-set; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska J., Smalins D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (Dec-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC018747; AAH18747.1; -  
 DR HSSP; P01861; 1ADQ.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-1-like.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF07654; C1-set; 3.  
 DR SMART; SM00409; IGV; 2.  
 DR SMART; SM00407; IGV; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D9 CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 470;  
 Best Local Similarity 97.9%; Pred. No. 4,6e-118;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNGALTSGVHTFPAVLQSS 60  
 141 ASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNGALTSGVHTFPAVLQSS 200

DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHRKSNLKVKPKESCDTHRCPCPAPPELLGG 120  
 201 GLYSLSVVTVPSSSLGTQTYICNVNHRKSNLKVKPKESCDTHRCPCPAPPELLGG 260

QY 201 GLYSLSVVTVPSSSLGTQTYICNVNHRKSNLKVKPKESCDTHRCPCPAPPELLGG 260  
 261 GLYSLSVVTVPSSSLGTQTYICNVNHRKSNLKVKPKESCDTHRCPCPAPPELLGG 320

DB 261 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAVKTKRPREQYN 320  
 321 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAVKTKRPREQYN 380

QY 321 STYRVSVTLTVLHQWMNNGEKYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 240  
 361 STYRVSVTLTVLHQWMNNGEKYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 300

DB 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSGVSFFLYSKLTVDKSRW 300  
 381 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSGVSFFLYSKLTVDKSRW 440

QY 381 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSGVSFFLYSKLTVDKSRW 440  
 441 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSGVSFFLYSKLTVDKSRW 470

DB 441 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSGVSFFLYSKLTVDKSRW 470

QY 441 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSGVSFFLYSKLTVDKSRW 470

RESULT 5  
 Q7ZSW1 PRELIMINARY; PRT; 470 AA.

AC Q7ZSW1;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 NCBI\_TaxID=9606;  
 RX NCBI\_TaxID=9606;  
 RA SEQUENCE FROM N.A.  
 RP TISSUE=Spleen;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Schein C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strusberg R.;  
RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC053984; AAHS3984.1; -.  
DR HSP; P01857; 1H2H.  
DR InterPro; IPR007110; IG-1like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
DR Hypothetical protein.  
KW SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 470;  
Best Local Similarity 97.9%; Pred. No. 4,6e-118;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTGSPSVPLAPSSKSTSGTAAAGCLVKDYFPEPVVSNMGSALTSGVHTFPAVLQSS 60  
DB 141 ASTGSPSVPLAPSSKSTSGTAAAGCLVKDYFPEPVVSNMGSALTSGVHTFPAVLQSS 200  
QY 61 GLYSLSVVTVSSSLGTQTYICNVNHRKSNLKVDKVEPKSCDKTHHCPCPAPPELLGG 120  
DB 201 GLYSLSVVTVSSSLGTQTYICNVNHRKSNLKVDKVEPKSCDKTHHCPCPAPPELLGG 260  
QY 121 PSVFLPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAVKTKRPEEYN 180  
DB 261 PSVFLPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAVKTKRPEEYN 320  
QY 181 STYRVSVLTVLHQMNGKEKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240  
DB 321 STYRVSVLTVLHQMNGKEKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 380  
QY 241 LTKNOVSLTCLVKGFPSPDIAVWESNQPENNNYKTPPVLDVSGSFFLYSKLTVDKSRW 300  
DB 381 LTKNOVSLTCLVKGFPSPDIAVWESNQPENNNYKTPPVLDVSGSFFLYSKLTVDKSRW 440  
QY 301 QOQNVFSCSVMEALAHNHQORSLSLSPGK 330  
DB 441 QOQNVFSCSVMEALAHNHQORSLSLSPGK 470

RESULT 6  
ID 06GMW7 PRELIMINARY; PRT; 475 AA.  
AC 06GMW7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_Taxid:9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Schein C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strusberg R.;  
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073782; AAH73782.1; -.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-1like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00407; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
DR Hypothetical protein.  
KW SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 475;  
Best Local Similarity 97.9%; Pred. No. 4,6e-118;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTGSPSVPLAPSSKSTSGTAAAGCLVKDYFPEPVVSNMGSALTSGVHTFPAVLQSS 60  
DB 146 ASTGSPSVPLAPSSKSTSGTAAAGCLVKDYFPEPVVSNMGSALTSGVHTFPAVLQSS 205  
QY 61 GLYSLSVVTVSSSLGTQTYICNVNHRKSNLKVDKVEPKSCDKTHHCPCPAPPELLGG 120  
DB 206 GLYSLSVVTVSSSLGTQTYICNVNHRKSNLKVDKVEPKSCDKTHHCPCPAPPELLGG 265  
QY 121 PSVFLPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAVKTKRPEEYN 180  
DB 266 PSVFLPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAVKTKRPEEYN 325  
QY 181 STYRVSVLTVLHQMNGKEKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240  
DB 326 STYRVSVLTVLHQMNGKEKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 385  
QY 241 LTKNOVSLTCLVKGFPSPDIAVWESNQPENNNYKTPPVLDVSGSFFLYSKLTVDKSRW 300

```
DB      386  LTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNKTTPPVLDSDGSFPLYSKLTVDKSRM 445
QY      301  OQGNVFSQSVMEALHNHYQKSLSPGK 330
DB      446  OQGNVFSQSVMEALHNHYQKSLSPGK 475

RESULT 7
Q6GMX1  PRELIMINARY; PRT; 476 AA.
AC      05-JUL-2004 (Tremblrel. 27, Created)
DT      05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT      05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxId=9606;
[1]
RN      SEQUENCE FROM N.A.
RP      TISSUE=Spleen;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN      SEQUENCE FROM N.A.
RP      TISSUE=Spleen;
RA      Strusberg R.;
RA      Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
DB      EMBL; BC073773; AAH7373.1; -.
DR      InterPro; IPR003599; IG.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003597; IG-cl.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG-v.
DR      Pfam; PF07654; Cl-sec; 3.
DR      Pfam; PF00047; Ig; 4.
DR      SMART; SM00409; IG; 2.
DR      SMART; SM00407; IGcl; 3.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG LIKE; 4.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KM      Hypothetical protein.
SQ      SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match      98.0%; Score 1729; DB 2; Length 476;
Best Local Similarity 97.9%; Pred. No. 4,6e-118;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1  ASTKGPSPVPLAPSSKSTSGTALGCLVDFPEPVTWSNGALITSGVHTFPAYLQSS 60
DB      147  ASTKGPSPVPLAPSSKSTSGTALGCLVDFPEPVTWSNGALITSGVHTFPAYLQSS 206
QY      61  GLYSLSVTVTPSSSLGTQTYICNVNHNKFSNTKVDKVEPKSCDKTHITCPCPAPPELLGG 120
```

```
DB      207  GLYSLSVTVTPSSSLGTQTYICNVNHNKFSNTKVDKVEPKSCDKTHITCPCPAPPELLGG 266
QY      121  PSVFLPFPKPDITLMSIRTPPEVTCVVDVSHEDPEVKENMYVDGVEVNAVTKTPREEQYN 180
DB      267  PSVFLPFPKPDITLMSIRTPPEVTCVVDVSHEDPEVKENMYVDGVEVNAVTKTPREEQYN 326
QY      181  STYRVSVTLTVLHQMWNNGKEKCVSNKALPAPTEKTSIRAKVQPREPQVYTLPPSRDE 240
DB      327  STYRVSVTLTVLHQMWNNGKEKCVSNKALPAPTEKTSIRAKVQPREPQVYTLPPSRDE 386
QY      241  LTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNKTTPPVLDSDGSFPLYSKLTVDKSRM 300
DB      387  LTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNKTTPPVLDSDGSFPLYSKLTVDKSRM 446
QY      301  OQGNVFSQSVMEALHNHYQKSLSPGK 330
DB      447  OQGNVFSQSVMEALHNHYQKSLSPGK 476

RESULT 8
Q6INT8  PRELIMINARY; PRT; 466 AA.
AC      06INT8;
DT      05-JUL-2004 (Tremblrel. 27, Created)
DT      05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT      05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE      IGHG1 protein.
GN      Name=IGHG1;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxId=9606;
[1]
RN      SEQUENCE FROM N.A.
RP      TISSUE=Peripheral Nervous System;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN      SEQUENCE FROM N.A.
RP      TISSUE=Peripheral Nervous System;
RA      Strusberg R.;
RA      Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
DB      EMBL; BC072419; AAH72419.1; -.
DR      HSSP; P01861; IADQ.
DR      InterPro; IPR003599; IG.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003597; IG-cl.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG-v.
DR      Pfam; PF07654; Cl-sec; 3.
DR      SMART; SM00409; IG; 2.
DR      SMART; SM00407; IGcl; 3.
DR      SMART; SM00406; IGV; 1.
```

DR PROSITE: PSS0835; IG\_LIKE; 4.  
DR PROSITE: PSS0290; IG\_MHC; UNKNOWN 2.  
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCEDEB1076E CRC64;

Query Match 97.8%; Score 1726; DB 2; Length 466;

Best Local Similarity 97.6%; Pred. No. 7,5e-118;

Matches 322; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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QY 1 ASTKGPVPEPLAPSSKSTSGGTAALGCLVKDYFPEPVVSNMGSALTSGVHTFPAVLQSS 60
DB 137 ASTKGPVPEPLAPSSKSTSGGTAALGCLVKDYFPEPVVSNMGSALTSGVHTFPAVLQSS 196
QY 61 GLYSLSVVTVPSSSLGTQTYICNNHKPSNTKVDKRPKSCDKHTHPCPCAPPELLGG 120
DB 197 GLYSLSVVTVPSSSLGTQTYICNNHKPSNTKVDKRPKSCDKHTHPCPCAPPELLGG 256
QY 121 PSVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKFMWYDGVENHNAKTKPREEQYN 180
DB 257 PSVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKFMWYDGVENHNAKTKPREEQYN 316
QY 181 STYRVSVLTVLHQMNMNGEKYCKVSNKALPAPIEKTISSKAKGPREQVYTLPPSRDE 240
DB 317 STYRVSVLTVLHQMNMNGEKYCKVSNKALPAPIEKTISSKAKGPREQVYTLPPSRDE 376
QY 241 LTRKNVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 377 LTRKNVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 436
QY 301 QQGNVFSCSVMHGALHNHYQKRSLSLSPGK 330
DB 437 QQGNVFSCSVMHGALHNHYQKRSLSLSPGK 466
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## RESULT 9

```
Q6N089 PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp666P15220.
GN Name=DKFZp666P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human CDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weill B., Amid C., Osanger A.,
RA Fobio G., Han M., Wiemann S.;
RA Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; B640627; CAE45781.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003559; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-sec; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN 2.
DR Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;
```

Query Match 97.8%; Score 1726; DB 2; Length 472;  
Best Local Similarity 97.6%; Pred. No. 7,6e-118;  
Matches 322; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```
QY 1 ASTKGPVPEPLAPSSKSTSGGTAALGCLVKDYFPEPVVSNMGSALTSGVHTFPAVLQSS 60
DB 143 ASTKGPVPEPLAPSSKSTSGGTAALGCLVKDYFPEPVVSNMGSALTSGVHTFPAVLQSS 202
QY 61 GLYSLSVVTVPSSSLGTQTYICNNHKPSNTKVDKRPKSCDKHTHPCPCAPPELLGG 120
DB 203 GLYSLSVVTVPSSSLGTQTYICNNHKPSNTKVDKRPKSCDKHTHPCPCAPPELLGG 262
QY 121 PSVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKFMWYDGVENHNAKTKPREEQYN 180
DB 263 PSVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKFMWYDGVENHNAKTKPREEQYN 322
QY 181 STYRVSVLTVLHQMNMNGEKYCKVSNKALPAPIEKTISSKAKGPREQVYTLPPSRDE 240
DB 323 STYRVSVLTVLHQMNMNGEKYCKVSNKALPAPIEKTISSKAKGPREQVYTLPPSRDE 382
QY 241 LTRKNVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 383 LTRKNVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 442
QY 301 QQGNVFSCSVMHGALHNHYQKRSLSLSPGK 330
DB 443 QQGNVFSCSVMHGALHNHYQKRSLSLSPGK 472
```

## RESULT 10

```
Q6P055 PRELIMINARY; PRT; 473 AA.
ID Q6P055;
AC Q6P055;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RG MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin I.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RA Submitted (Jan-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH65820.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003559; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
```

DR Pfam: PF07654; Cl-set: 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IG; 3.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 473;  
 Best Local Similarity 97.6%; Pred. No. 9e-118;  
 Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKPSVFPLPASPSSKSTSGGTAALGCLVKDYFPEPVVTSNMSGALITSGVHTFPVAVLQSS 60  
 DB 144 ASTKPSVFPLPASPSSKSTSGGTAALGCLVKDYFPEPVVTSNMSGALITSGVHTFPVAVLQSS 203  
 QY 61 GLYSLSVVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDTHTCPCPAPABELLGG 120  
 DB 204 GLYSLSVVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDTHTCPCPAPABELLGG 263  
 QY 121 PSVFLPPEPKDQTLMISTRPEVTCVVVDVSHEDPEVKFMWYVDGVEVHNNAKTKPREEQYN 180  
 DB 264 PSVFLPPEPKDQTLMISTRPEVTCVVVDVSHEDPEVKFMWYVDGVEVHNNAKTKPREEQYN 323  
 QY 181 STYRVVSVLTVLHQQWMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240  
 DB 324 STYRVVSVLTVLHQQWMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 383  
 QY 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDVSGSFYLSKLTVDKSRW 300  
 DB 384 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDVSGSFYLSKLTVDKSRW 443  
 QY 301 QQGNVFSCSVHMEALHNHYQQRSLSLSPGK 330  
 DB 444 QQGNVFSCSVHMEALHNHYTQKSLSLSPGK 473

RESULT 11

Q6MZ06 PRELIMINARY; PRT; 475 AA.

AC Q6MZ06;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Hypothetical protein DKFZp686G1190.  
 GN Name=DKFZp686G1190;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human esophagus tumor;  
 RG The German Human CDNA Consortium;  
 RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,  
 RA Han M., Wiemann S.;  
 RA Submitted (Aug-2003) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; BX640947; CAE45972.1; --  
 DR HSSP; P01861; IADO.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IG; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 475;  
 Best Local Similarity 97.6%; Pred. No. 9e-118;  
 Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKPSVFPLPASPSSKSTSGGTAALGCLVKDYFPEPVVTSNMSGALITSGVHTFPVAVLQSS 60  
 DB 146 ASTKPSVFPLPASPSSKSTSGGTAALGCLVKDYFPEPVVTSNMSGALITSGVHTFPVAVLQSS 205  
 QY 61 GLYSLSVVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDTHTCPCPAPABELLGG 120  
 DB 206 GLYSLSVVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDTHTCPCPAPABELLGG 265  
 QY 121 PSVFLPPEPKDQTLMISTRPEVTCVVVDVSHEDPEVKFMWYVDGVEVHNNAKTKPREEQYN 180  
 DB 266 PSVFLPPEPKDQTLMISTRPEVTCVVVDVSHEDPEVKFMWYVDGVEVHNNAKTKPREEQYN 325  
 QY 181 STYRVVSVLTVLHQQWMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240  
 DB 326 STYRVVSVLTVLHQQWMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 385  
 QY 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDVSGSFYLSKLTVDKSRW 300  
 DB 386 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDVSGSFYLSKLTVDKSRW 445  
 QY 301 QQGNVFSCSVHMEALHNHYQQRSLSLSPGK 330  
 DB 446 QQGNVFSCSVHMEALHNHYTQKSLSLSPGK 475

RESULT 12

Q6N094 PRELIMINARY; PRT; 480 AA.

AC Q6N094;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Hypothetical protein DKFZp686O01196.  
 GN Name=DKFZp686O01196;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human esophagus tumor;  
 RG The German Human CDNA Consortium;  
 RA Mambut R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RA Submitted (Aug-2003) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; BX640622; CAE45776.1; --  
 DR HSSP; P01861; IADO.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IG; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 480;  
 Best Local Similarity 97.6%; Pred. No. 9.2e-118;  
 Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKPSVFPLPASPSSKSTSGGTAALGCLVKDYFPEPVVTSNMSGALITSGVHTFPVAVLQSS 60  
 DB 151 ASTKPSVFPLPASPSSKSTSGGTAALGCLVKDYFPEPVVTSNMSGALITSGVHTFPVAVLQSS 210



QY 61 GLYSSSVTVVSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTPCPCPAPELLGG 120  
DB 211 GLYSSSVTVVSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTPCPCPAPELLGG 270  
QY 121 PSVFLFPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFMVYDGVFNHAKTKPREEOYN 180  
DB 271 PSVFLFPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFMVYDGVFNHAKTKPREEOYN 330  
QY 181 STYRVSVTLTVLHOMNMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPOVYTLPPSRDE 240  
DB 331 STYRVSVTLTVLHOMNMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPOVYTLPPSRDE 390  
QY 241 LTKNOVSLTCLVKGFPYPSDIAVEMESNGPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300  
DB 391 LTKNOVSLTCLVKGFPYPSDIAVEMESNGPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 450  
QY 301 OOGNVFSCSVMEHGLHNHYTKSLSPGK 330  
DB 451 OOGNVFSCSVMEHGLHNHYTKSLSPGK 480

## RESULT 13

ID 06N097 PRELIMINARY; PRT; 481 AA.  
AC 06N097;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp668H20196.  
OS Homo sapiens (Human).  
GN Name=DKFZp668H20196;  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominda; Homo.  
OX NCBI\_Taxid=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human esophagus tumor;  
RG The German Human CDNA Consortium;  
RA Wambert R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.,  
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640619; CAE45773.1; -  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; Ig\_2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 481 AA; 52759 MW; 47220D9E64BDF98B CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 481;  
Best Local Similarity 97.6%; Pred. No. 9.2e-118;  
Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKGSVPPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60  
DB 152 ASTKGSVPPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 211  
QY 61 GLYSSSVTVVSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTPCPCPAPELLGG 120  
DB 212 GLYSSSVTVVSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTPCPCPAPELLGG 271  
QY 121 PSVFLFPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFMVYDGVFNHAKTKPREEOYN 180  
DB 272 PSVFLFPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFMVYDGVFNHAKTKPREEOYN 331

QY 181 STYRVSVTLTVLHOMNMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPOVYTLPPSRDE 240  
DB 332 STYRVSVTLTVLHOMNMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPOVYTLPPSRDE 391  
QY 241 LTKNOVSLTCLVKGFPYPSDIAVEMESNGPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300  
DB 392 LTKNOVSLTCLVKGFPYPSDIAVEMESNGPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 451  
QY 301 OOGNVFSCSVMEHGLHNHYTKSLSPGK 330  
DB 452 OOGNVFSCSVMEHGLHNHYTKSLSPGK 481

## RESULT 14

ID 07Z351 PRELIMINARY; PRT; 482 AA.  
AC 07Z351;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Hypothetical protein DKFZp66N02209.  
OS Homo sapiens (Human).  
GN Name=DKFZp66N02209;  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominda; Homo.  
OX NCBI\_Taxid=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RG Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.,  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX538118; CAD98026.1; -  
DR HSSP; P01857; 1H2H.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 482;  
Best Local Similarity 97.6%; Pred. No. 9.2e-118;  
Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKGSVPPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60  
DB 153 ASTKGSVPPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 212  
QY 61 GLYSSSVTVVSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTPCPCPAPELLGG 120  
DB 213 GLYSSSVTVVSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTPCPCPAPELLGG 272  
QY 121 PSVFLFPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFMVYDGVFNHAKTKPREEOYN 180  
DB 273 PSVFLFPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFMVYDGVFNHAKTKPREEOYN 332  
QY 181 STYRVSVTLTVLHOMNMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPOVYTLPPSRDE 240  
DB 333 STYRVSVTLTVLHOMNMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPOVYTLPPSRDE 392  
QY 241 LTKNOVSLTCLVKGFPYPSDIAVEMESNGPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300  
DB 393 LTKNOVSLTCLVKGFPYPSDIAVEMESNGPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 452  
QY 301 OOGNVFSCSVMEHGLHNHYTKSLSPGK 330  
DB 453 OOGNVFSCSVMEHGLHNHYTKSLSPGK 482

```
RESULT 15
O6N096 PRELIMINARY: PRT: 466 AA.
ID O6N096 AC O6N096:
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp681i15196.
GN Name=DKFZp681i15196;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RA Wamburt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fodor G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640620; CAB4574.1; -.
DR HSSP; P01861; IADO.
DR InterPro; IPR003559; IG.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein
SQ SEQUENCE 466 AA; 50926 MW; 01E91B748D6D57C4 CRC64;

Query Match 97.6%; Score 1722; DB 2; Length 466;
Best Local Similarity 97.3%; Pred.No.1.5e-117;
Matches 321; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPPVTVSNVSGALTSGVHTFPAVLQSS 60
DB 137 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPPVTVSNVSGALTSGVHTFPAVLQSS 196
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCTPCPAPRLGG 120
DB 197 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCTPCPAPRLGG 256
QY 121 PSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEHNHVKTKPREEQYN 180
DB 257 PSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEHNHVKTKPREEQYN 316
QY 161 STYRVVSUTLVHQNMMNGEKYCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240
DB 317 STYRVVSUTLVHQNMMNGEKYCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 376
QY 241 LTKNOVSLTCLVKGFYPSDIAVEMESNGOPENNYKTPPVLDVSGSFLLYSKLTVDKSRW 300
DB 377 LTKNOVSLTCLVKGFYPSDIAVEMESNGOPENNYKTPPVLDVSGSFLLYSKLTVDKSRW 436
QY 301 QQGNVFSCSVMEALHNHYQORSLSLSPGK 330
DB 437 QQGNVFSCSVMEALHNHYQORSLSLSPGK 466
```

Search completed: June 7, 2005, 09:01:27  
Job time : 165.435 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 08:38:56 ; Search time 167.565 Seconds

(without alignments)  
761.681 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764

Sequence: 1 ASTKCPVFPPLAPSSKSTSG.....MHEALHNHYQKSLSPCK 330

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp19808:\*

#### SUMMARIES

Result No. Score Query Match Length DB ID Description

1	1764	100.0	330	6	AAO19664	AAO19664 Human IgG
2	1729	98.0	330	4	AAO4071	AAO4071 ZCytoc 10
3	1729	98.0	330	5	AAO47856	AAO47856 Human Ig-
4	1729	98.0	330	5	AAE21960	AAE21960 Human dea
5	1729	98.0	330	5	ABH81641	ABH81641 Human IgG
6	1729	98.0	330	5	ABH805736	ABH805736 Human imm
7	1729	98.0	330	6	ABP71856	ABP71856 Human IgG
8	1729	98.0	330	6	AAE32915	AAE32915 Human imm
9	1729	98.0	330	6	AAE32627	AAE32627 Human imm
10	1729	98.0	330	6	ABR82103	ABR82103 Human DR6
11	1729	98.0	330	6	AAO31102	AAO31102 Human A2-
12	1729	98.0	330	6	ABR55836	ABR55836 Anti-Ang-
13	1729	98.0	330	6	AAO30893	AAO30893 Human imm
14	1729	98.0	330	7	ADF11389	ADF11389 Anti-OPGL
15	1729	98.0	330	7	ADG97351	ADG97351 Human IgG
16	1729	98.0	330	7	ADG93605	ADG93605 Cytokine
17	1729	98.0	330	7	ADF75001	ADF75001 Human Ig
18	1729	98.0	330	8	ADM41537	ADM41537 Anti-Inte
19	1729	98.0	330	8	ADM68911	ADM68911 Human IgG
20	1729	98.0	330	8	ADR43460	ADR43460 Heavy cha
21	1729	98.0	330	8	ADR31605	ADR31605 Human IgG
22	1729	98.0	330	8	ADG87909	ADG87909 Anti-IFN-
23	1729	98.0	330	8	ADN33230	ADN33230 IgG1-CH h
24	1729	98.0	330	8	ADG94906	ADG94906 Anti-IFN-
25	1729	98.0	332	8	ADL35095	ADL35095 Human IgG

26	1729	98.0	333	8	ADJ95912	ADJ95912 Human IgG
27	1729	98.0	333	8	ADL22761	ADL22761 Human ant
28	1729	98.0	351	2	AAE43685	AAE43685 Human kap
29	1729	98.0	356	8	ADJ95976	ADJ95976 Immunoglo
30	1729	98.0	371	1	AAE91918	AAE91918 Sequence
31	1729	98.0	442	6	ABR39465	ABR39465 Humanised
32	1729	98.0	442	6	ABR39474	ABR39474 Humanised
33	1729	98.0	442	6	ABU08311	ABU08311 Humanised
34	1729	98.0	442	6	ABU08320	ABU08320 Humanised
35	1729	98.0	442	6	ABR39793	ABR39793 Humanised
36	1729	98.0	442	6	ABR80113	ABR80113 Deglycosy
37	1729	98.0	442	6	ABR80109	ABR80109 Heavy cha
38	1729	98.0	442	7	ADG94066	ADG94066 Humanised
39	1729	98.0	442	7	ADG94075	ADG94075 Humanised
40	1729	98.0	442	7	ADN61714	ADN61714 Humanised
41	1729	98.0	444	6	AAE35327	AAE35327 Humanised
42	1729	98.0	444	6	AAE34876	AAE34876 B1W4/8 a
43	1729	98.0	444	8	ADL15443	ADL15443 Humanised
44	1729	98.0	444	8	ADU00851	ADU00851 Humanised
45	1729	98.0	445	6	AAO31101	AAO31101 Human A2-

#### ALIGNMENTS

RESULT 1  
AAO19664  
ID AAO19664 standard; protein; 330 AA.  
AC AAO19664;  
AD 28-MAR-2003 (first entry)  
DE Human IgG1 heavy chain constant region.  
XX  
XX Human; IgG1; immunoglobulin G; immunotherapy; immune disease;  
XX Fc epsilon receptor; autoimmune disease; constant region; heavy chain;  
XX antiaesthetic; antiallergic; antiinflammatory; dermatological;  
XX antiarthritic; antirheumatic; antidiabetic; neuroprotective.  
OS Homo sapiens.  
XX  
XX WO200288317-A2.  
XX  
XX PD 07-NOV-2002.  
XX  
XX PF 01-MAY-2002; 2002WO-US013527.  
XX  
XX PR 01-MAY-2001; 2001US-00847208.  
XX PR 24-OCT-2001; 2001US-0000439.  
XX  
XX PA (REGC ) UNIV CALIFORNIA.  
XX  
XX PI Saxon A, Zhang K, Zhu D;  
XX WPI; 2003-103456/09.  
XX  
XX DR New fusion molecules comprising polypeptide sequences that bind to IgG  
XX PT Inhibitory receptor and native IgG receptor, useful for treating IgE-  
XX PT mediated hypersensitivity reactions, e.g. asthma or allergies, or  
XX PT autoimmune diseases.  
XX  
XX PS Claim 64; Fig 2; 116pp; English.  
XX  
XX CC The present invention relates to a fusion molecule comprising a first  
XX CC polypeptide sequence capable of specific binding to a native IgG  
XX CC inhibitory receptor consisting of an immune receptor tyrosine-based  
XX CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
XX CC functionally connected to a second polypeptide sequence capable of  
XX CC specific binding directly or indirectly to a native IgG receptor  
XX CC (Fc epsilonR). Also provided are nucleotide sequences encoding such a  
XX CC fusion protein. The fusion molecules and compositions are useful for  
XX CC treating an IgE-mediated biological response, preferably an IgE-mediated

CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,  
CC or symptoms resulting from, a type I hypersensitivity reaction in a  
CC subject receiving immunotherapy. The present sequence is the human IgG1  
CC heavy chain constant region  
XX  
SQ Sequence 330 AA;  
Query Match 100.0%; Score 1764; DB 6; Length 330;  
Best Local Similarity 100.0%; Pred. No. 4e-125;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ASTKGPSPVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
DB 1 ASTKGPSPVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
QY 61 GLYSLSVVTVSPSSSLGTQTYICNVNHRKSNTRVKDKVPEPKSCDKHTHTCPCPAPPELLGG 120  
DB 61 GLYSLSVVTVSPSSSLGTQTYICNVNHRKSNTRVKDKVPEPKSCDKHTHTCPCPAPPELLGG 120  
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENHVKTKRPREQYN 180  
DB 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENHVKTKRPREQYN 180  
QY 181 STYRVVSVLTVLHQMNWNGEKYCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240  
DB 181 STYRVVSVLTVLHQMNWNGEKYCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240  
QY 241 LRKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGFPLYSKLTVDKSRW 300  
DB 241 LRKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGFPLYSKLTVDKSRW 300  
QY 301 QOQNVFSCSVMEBALHNHYQQRSLSLSPGK 330  
DB 301 QOQNVFSCSVMEBALHNHYQQRSLSLSPGK 330  
RESULT 2  
AAB04071 ID AAB04071 standard; protein; 330 AA.  
XX AAB04071;  
DT 11-APR-2001 (first entry)  
XX Zcytor 10::Igg gamma fusion peptide.  
DE Zcytor 10::Igg gamma fusion peptide.  
XX zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;  
KM binding; detection; modulation; recombinant cell; haematopoietic cell;  
KW lymphoid cell; myeloid cell; lymph; immune system; blood; bone;  
XX inflammatory response; inflammation; spleen; human.  
OS Synthetic.  
OS Homo sapiens.  
PN WO200068381-A1.  
XX 16-NOV-2000.  
XX 11-MAY-2000; 2000MO-US012924.  
XX PF 11-MAY-1999; 99US-00309861.  
XX PR 11-MAY-1999;  
XX (ZYMO ) ZYMOGENETICS INC.  
XX PA Presnell SR, Foester DC, Hammond AK, Lok S;  
XX PI WPI; 2001-016096/02.  
XX DR N-PSDB; AAA54473.  
XX KW New cytokine receptor mouse zcytor 10, useful for detecting ligands that

PT stimulate proliferation or development of hematopoietic, lymphoid and  
PT myeloid cells.  
XX Example 17; Page 120-121; 134pp; English.  
XX Isolating a nucleotide which encodes the zcytor 10 cytokine receptor  
CC enables the production of recombinant cells expressing the receptor.  
CC Those cells can then be used to detect the presence of a modulator of  
CC zcytor10 protein by culturing the cells in the presence of a test ligand  
CC and comparing levels of activity of mouse zcytor10 in the presence and  
CC absence of the test sample. Similarly, detection of zcytor10 receptor  
CC ligand within a test sample can be achieved. The method comprising  
CC contacting a test sample containing an amino acid sequence from Cys45 or  
CC Gly25 to Pro230 of the zcytor 10 cytokine receptor and detecting the  
CC binding of the polypeptide to a ligand in the sample. Specified peptide  
CC fragments of the zcytor 10 cytokine receptor and the methods described  
CC are used to identify ligands that stimulate the proliferation and/or  
CC development of hematopoietic, lymphoid and myeloid cells. Peptide  
CC fragments of the cytokine receptor are useful for treating lymphoid,  
CC immune, inflammatory, splenic, blood or bone disorders and for generating  
CC antibodies directed against the receptor. A vector expressing a secreted  
CC human zcytor 10 heterodimer is constructed. In this construct the  
CC extracellular cytokine binding domain of zcytor 10 is fused to the heavy  
CC chain of IgG gamma and the extracellular portion of the the heteromeric  
CC cytokine receptor subunit (an interleukin receptor subunit) is fused to  
CC human kappa light chain (see GENESEQ record AAA54474). The two sequences  
CC are fused together using two primers (AAA54475, AAA54476)  
XX  
SQ Sequence 330 AA;  
Query Match 98.0%; Score 1729; DB 4; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 ASTKGPSPVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
DB 1 ASTKGPSPVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
QY 61 GLYSLSVVTVSPSSSLGTQTYICNVNHRKSNTRVKDKVPEPKSCDKHTHTCPCPAPPELLGG 120  
DB 61 GLYSLSVVTVSPSSSLGTQTYICNVNHRKSNTRVKDKVPEPKSCDKHTHTCPCPAPPELLGG 120  
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENHVKTKRPREQYN 180  
DB 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENHVKTKRPREQYN 180  
QY 181 STYRVVSVLTVLHQMNWNGEKYCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240  
DB 181 STYRVVSVLTVLHQMNWNGEKYCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240  
QY 241 LRKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGFPLYSKLTVDKSRW 300  
DB 241 LRKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGFPLYSKLTVDKSRW 300  
QY 301 QOQNVFSCSVMEBALHNHYQQRSLSLSPGK 330  
DB 301 QOQNVFSCSVMEBALHNHYQQRSLSLSPGK 330  
RESULT 3  
AAM47856 ID AAM47856 standard; protein; 330 AA.  
XX AAM47856;  
XX 22-FEB-2002 (first entry)  
XX Human Ig-gamma1 heavy chain constant region amino acid sequence.  
XX Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;  
XX Human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;  
XX transgenic plant.



CC recuperation from chemotherapy, recuperation from irradiation therapy, or  
CC a condition or symptom related to the above mentioned diseases in a  
CC mammal. The present sequence is human DR6 protein-related protein  
XX  
XX  
SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 5; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKPSVPEPLAPSSKSTSGTAAAGCLVKDYFPEPVYVSNMNSGALTSGVHTFPAVLQSS 60  
DB 1 ASTKPSVPEPLAPSSKSTSGTAAAGCLVKDYFPEPVYVSNMNSGALTSGVHTFPAVLQSS 60  
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHPCPCPAPELLGG 120  
DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHPCPCPAPELLGG 120  
QY 121 PSVFLPPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVENNAKTRPREQYN 180  
DB 121 PSVFLPPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVENNAKTRPREQYN 180  
QY 181 STYRVSVLTVLHQMNMNGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240  
DB 181 STYRVSVLTVLHQMNMNGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240  
QY 241 LTRNQVSLTCLVKGFPYPSDIAVEMESNGCPENNYKTPPVLDVSGSFYLSKLTVDKSRW 300  
DB 241 LTRNQVSLTCLVKGFPYPSDIAVEMESNGCPENNYKTPPVLDVSGSFYLSKLTVDKSRW 300  
QY 301 OQGNVFSCSVMEALHNHYQKRSLSLSPGK 330  
DB 301 OQGNVFSCSVMEALHNHYQKRSLSLSPGK 330

RESULT 5  
ABB81641  
ID ABB81641 standard; protein; 330 AA.

AC ABB81641;  
XX  
DT 25-SEP-2002 (first entry)

DE Human IgG gamma 1 heavy chain SEQ ID NO:15.

XX Human; zcytor19; cytokine receptor; immunosuppressive; cytostatic;  
XX antirheumatic; antiarthritic; neuroprotective; anti-HIV; haemostatic;  
XX antidiabetic; nephrotoxic; dermatological; anti-HIV; haemostatic;  
XX vaccine; immune system; T-cell specific leukemia; lymphoma; lupus;  
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis; HIV;  
XX diabetes mellitus; inflammatory bowel disease; Crohn's disease; asthma;  
XX immunologic renal disease; glomerulonephritis; vasculitis; polyarteritis;  
XX mesangiol proliferative disease; chronic lymphocytic leukaemia; bronchitis;  
XX secondary glomerulonephritis; scleroderma; amyloidosis; multiple myeloma;  
XX haemolytic uremic syndrome; renal neoplasm; urological neoplasm;  
XX emphysema; chronic airway disease.

XX Homo sapiens.

OS WO200244209-A2.

PN 06-JUN-2002.

PF 28-NOV-2001; 2001WO-US044808.

PR 28-NOV-2000; 2000US-0253561P.

PR 07-FEB-2001; 2001US-0267211P.

XX (ZYMO ) ZYMOGENETICS INC.

XX Presnell SR, Xu W, Novak JE, Whitmore TE, Grant FJ;

XX WPI; 2002-527700/56.

DR N-PSDB; ABQ73076.

XX Novel Zcytor19 polypeptides and polynucleotides useful for stimulating  
XX immune responses in animals for producing antibodies, and for treating  
XX autoimmune diseases, leukemia and asthma.

PS Example 7; Page 171-172; 200pp; English.

XX The present invention describes an isolated human zcytor19 protein (I),  
XX and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic,  
XX antirheumatic, antiarthritic, neuroprotective, anti-HIV and haemostatic,  
XX antidiabetic, nephrotoxic, dermatological, anti-HIV and haemostatic  
XX activities, and can be used in vaccines. (I) or an antibody binding (I)  
XX can be used for suppressing the immune system for reducing rejection of  
XX tissue or organ transplants and grafts and for treating T-cell specific  
XX leukaemias or lymphomas and autoimmune diseases including rheumatoid  
XX arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel  
XX disease and Crohn's disease. The antibodies can also be used for treating  
XX immunologic renal diseases, glomerulonephritis, mesangiol proliferative  
XX disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or  
XX vasculitis associated with lupus, polyarteritis, scleroderma, HIV-related  
XX diseases, amyloidosis and haemolytic uraemic syndrome. (I) and the  
XX antibodies can also be used for renal or urological neoplasms and  
XX multiple myelomas, asthma, bronchitis, emphysema and other chronic airway  
XX diseases. Human zcytor19 is located to chromosome 1, more specifically to  
XX chromosome 1p36.11. The present sequence represents a human IgG gamma 1  
XX heavy chain protein, which is used in an example from the present  
XX invention

SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 5; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKPSVPEPLAPSSKSTSGTAAAGCLVKDYFPEPVYVSNMNSGALTSGVHTFPAVLQSS 60  
DB 1 ASTKPSVPEPLAPSSKSTSGTAAAGCLVKDYFPEPVYVSNMNSGALTSGVHTFPAVLQSS 60  
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHPCPCPAPELLGG 120  
DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHPCPCPAPELLGG 120  
QY 121 PSVFLPPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVENNAKTRPREQYN 180  
DB 121 PSVFLPPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVENNAKTRPREQYN 180  
QY 181 STYRVSVLTVLHQMNMNGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240  
DB 181 STYRVSVLTVLHQMNMNGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240  
QY 241 LTRNQVSLTCLVKGFPYPSDIAVEMESNGCPENNYKTPPVLDVSGSFYLSKLTVDKSRW 300  
DB 241 LTRNQVSLTCLVKGFPYPSDIAVEMESNGCPENNYKTPPVLDVSGSFYLSKLTVDKSRW 300  
QY 301 OQGNVFSCSVMEALHNHYQKRSLSLSPGK 330  
DB 301 OQGNVFSCSVMEALHNHYQKRSLSLSPGK 330

RESULT 6  
ABB05736  
ID ABB05736 standard; protein; 330 AA.

AC ABB05736;

DT 01-MAY-2002 (first entry)

XX Human immunoglobulin G gamma 1 protein sequence SEQ ID NO:38.

XX Zcytor17; chromosome 5; Sg11; cytokine receptor; immunomodulatory;  
XX antirheumatic; antiarthritic; neuroprotective; cytostatic;  
XX muscular; lymphoid; immune; inflammatory; splenic; blood; bone;



infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease.

Homo sapiens.

WO200200721-A2.

03-JAN-2002.

26-JUN-2001; 2001WO-US020484.

26-JUN-2000; 2000US-0214282P.

29-JUN-2000; 2000US-0214955P.

08-FEB-2001; 2001US-0267963P.

(ZYMO) ZYMOGENETICS INC.

Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL, Maurer MF;

MP1; 2002-090519/12.

N-PSDB; ABA93797.

Isolated polynucleotide encoding a cytokine receptor zcytor17 which is useful for treating and diagnosing lymphoid, immune, inflammatory, splenic, blood or bone disorders.

Example 17; Page 187-188; 235pp; English.

The present invention describes a cytokine receptor designated zcytor17. Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, antirheumatic, antiarthritic and muscular activities. The zcytor17 proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, splenic, blood or bone disorders. Agonists or anti-zcytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral infections. They are also useful for inducing cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to ABA93843 and ABB05730 to ABB05745 represent sequences used in the exemplification of the present invention

Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 5; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 ASTKGSVPFLPABSSKSTSGTALGCLVKDYFPEPVTVSWNSGALTSGVHTPFAVLQSS 60  
1 ASTKGSVPFLPABSSKSTSGTALGCLVKDYFPEPVTVSWNSGALTSGVHTPFAVLQSS 60

61 GLYSLSVVTVBSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKHTHTCPPCPAPRLGG 120  
61 GLYSLSVVTVBSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKHTHTCPPCPAPRLGG 120

121 PSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAVKTPREBOYN 180  
121 PSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAVKTPREBOYN 180

181 STYRVSVTLTVLHQMNMNGEKYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240  
181 STYRVSVTLTVLHQMNMNGEKYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240

241 LTNQVSLTCLVVGFPSPDIAVWESNGQPENNYKTPPILDSVGSFRLLYSKLTVDKSRW 300  
241 LTNQVSLTCLVVGFPSPDIAVWESNGQPENNYKTPPILDSVGSFRLLYSKLTVDKSRW 300

301 QCGNVPSCVWHEALHNHYQSRSLSPCK 330  
301 QCGNVPSCVWHEALHNHYQSRSLSPCK 330

RESULT 7  
ID ABP71856 standard; protein; 330 AA.  
AC ABP71856;  
DT 17-APR-2003 (first entry)  
DE Human IgG1 Fcgamma region.  
KW Human; fusion protein; IgE Fcepsilon; IgG Fcgamma; FcepsilonRI; allergy; allergic asthma; allergic rhinitis; hay fever; food allergy;  
KW atopic dermatitis; drug allergy; peanut allergen.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Region 1..98  
FT Region /label= CH1 region  
FT Region 99..113  
FT Region /label= Hinge\_region  
FT Region 114..223  
FT Region /label= CH2\_region  
FT Region 224..330  
FT Region /label= CH3\_region  
PN WO2002102320-A2.  
PD 27-DEC-2002.  
PF 14-JUN-2002; 2002WO-US019448.  
PF 15-JUN-2001; 2001US-0298710P.  
PR (TANO-) TANOX INC.  
PA An L, Wu H, Fung MSC;  
PI WPI; 2003-167440/16.  
DR New fusion protein which binds to FcepsilonRI or RI1 receptor and FcgammaRIIb receptor, useful for treating or preventing allergies and asthma, comprises an IgE Fcepsilon fragment and an IgG Fcgamma fragment.  
PS Disclosure; Fig 5; 32pp; English.  
XX The invention relates to a novel fusion protein comprising an IgE Fcepsilon fragment and an IgG Fcgamma fragment, which binds to an FcepsilonRI and/or FcepsilonRII receptor and an FcgammaRIIb receptor. The fusion protein of the invention may have a use in protein therapy. The fusion protein is useful in treating or preventing IgE-mediated allergies and asthma, such as allergic asthma, allergic rhinitis, hay fever, food allergy, atopic dermatitis and drug allergy. The allergic response is particularly caused by peanut allergen. The present sequence represents the human IgG1 Fcgamma fragment

Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 6; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 ASTKGSVPFLPABSSKSTSGTALGCLVKDYFPEPVTVSWNSGALTSGVHTPFAVLQSS 60  
1 ASTKGSVPFLPABSSKSTSGTALGCLVKDYFPEPVTVSWNSGALTSGVHTPFAVLQSS 60

61 GLYSLSVVTVBSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKHTHTCPPCPAPRLGG 120  
61 GLYSLSVVTVBSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKHTHTCPPCPAPRLGG 120

```
Db 61 GYSSLSVTVTPSSSLGQTYICNVNHNKSNKVDKKEPKSCDKTHTCPPEAPPELLGG 120
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENMYVDGVEVHNVTKRPREEQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENMYVDGVEVHNVTKRPREEQYN 180
Qy 181 STYRVAVSVLTVLHQMNLNGKEYKCKVSNKALPAPIEKTISAKVQPREPQVYTLPPSRDE 240
Db 181 STYRVAVSVLTVLHQMNLNGKEYKCKVSNKALPAPIEKTISAKVQPREPQVYTLPPSRDE 240
Qy 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFLLYSKLTVDKSRM 300
Db 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFLLYSKLTVDKSRM 300
Qy 301 QQGNVFSCSVMEALHNHYQQRSLSPGK 330
Db 301 QQGNVFSCSVMEALHNHYQQRSLSPGK 330
```

## RESULT 8

AAE32915  
ID AAE32915 standard; protein; 330 AA.

AC AAE32915;

XX 24-MAR-2003 (first entry)

DT Human immunoglobulin G1 (IgG1) heavy chain Fc region.

XX T-cell; immunogenic; therapy; human; immunoglobulin G1; IgG1.

KW Homo sapiens.

OS WO200279232-A2.

XX 10-OCT-2002.

PD 30-MAR-2002; 2002WO-US009815.

XX 30-MAR-2001; 2001US-0280625P.

XX (LEXI-) LEXIGEN PHARM CORP.

XX G111ies SD;

PI WPI; 2003-103259/09.

DR Reducing the immunogenicity of a fusion protein comprises changing an amino acid within the junction region to reduce the ability of the candidate T-cell epitope identified within the junction spanning to interact with T-cell receptor.

PS Disclosure; Page 49-50; 68pp; English.

XX The invention relates to a method for reducing the immunogenicity of a fusion protein which involves identifying a candidate T-cell epitope within a junction spanning a fusion junction of a fusion protein, and changing an amino acid within the junction region to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor. The method is useful for reducing the immunogenicity of a fusion protein. It is useful for analysing, changing or modifying one or more amino acids in the junction region of a fusion protein to identify a T-cell epitope and reduce its ability to interact with a T-cell receptor. The less immunogenic fusion proteins are useful in providing therapeutic treatment. The present sequence is human immunoglobulin G1 (IgG1) heavy chain Fc region used to illustrate the method of the invention

XX Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 6; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy 1 ASTKPSVPEPLAPSSKSTSGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHPFPAVLQSS 60
Db 1 ASTKPSVPEPLAPSSKSTSGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHPFPAVLQSS 60
Qy 61 GYSSLSVTVTPSSSLGQTYICNVNHNKSNKVDKKEPKSCDKTHTCPPEAPPELLGG 120
Db 61 GYSSLSVTVTPSSSLGQTYICNVNHNKSNKVDKKEPKSCDKTHTCPPEAPPELLGG 120
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENMYVDGVEVHNVTKRPREEQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENMYVDGVEVHNVTKRPREEQYN 180
Qy 181 STYRVAVSVLTVLHQMNLNGKEYKCKVSNKALPAPIEKTISAKVQPREPQVYTLPPSRDE 240
Db 181 STYRVAVSVLTVLHQMNLNGKEYKCKVSNKALPAPIEKTISAKVQPREPQVYTLPPSRDE 240
Qy 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFLLYSKLTVDKSRM 300
Db 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFLLYSKLTVDKSRM 300
Qy 301 QQGNVFSCSVMEALHNHYQQRSLSPGK 330
Db 301 QQGNVFSCSVMEALHNHYQQRSLSPGK 330
```

## RESULT 9

AAE32627  
ID AAE32627 standard; protein; 330 AA.

AC AAE32627;

XX 24-MAR-2003 (first entry)

DT Human immunoglobulin G1 (IgG1) heavy chain Fc region.

XX Human; immunogenic; therapy; immunoglobulin G1; IgG1.

KW Homo sapiens.

OS WO200279415-A2.

XX 10-OCT-2002.

PD 29-MAR-2002; 2002WO-US009650.

XX 30-MAR-2001; 2001US-0280625P.

XX (LEXI-) LEXIGEN PHARM CORP.

XX G111ies SD;

PI WPI; 2003-111794/10.

DR Reducing the immunogenicity of a fusion protein by changing an amino acid within the junction region spanning a fusion junction of a fusion protein to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor.

PS Disclosure; Page 49-50; 67pp; English.

XX The present invention relates to a method of reducing the immunogenicity of a fusion protein. The method involves identifying a candidate T-cell epitope within a junction region spanning a fusion junction of a fusion protein and changing an amino acid within the junction region to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor. The method is useful for reducing the immunogenicity of fusion proteins for use in therapy. The present sequence is human immunoglobulin G1 (IgG1) heavy chain Fc region. This sequence is used to illustrate the method of the invention

XX Sequence 330 AA;

Query Match	98.0%	Score 1729	DB 6	Length 330
Best Local Similarity	97.9%	Pred. No. 1.8e-122		
Matches 323	Conservative 3	Mismatches 4	Indels 0	Gaps 0
QY	1	ASTGPGSPFLPAPSSKTSNGGTAALGCLVKQFPEPPVTVSNMSGALTSGVHTFPAPVLQSS	60	
DB	1	ASTGPGSPFLPAPSSKTSNGGTAALGCLVKQFPEPPVTVSNMSGALTSGVHTFPAPVLQSS	60	
QY	61	GLYSLSSTVAVTPSSSLGTQTYICNVNHRKPSNTKVDPKSPKSCDKTHITCPCPAPELLGG	120	
DB	61	GLYSLSSTVAVTPSSSLGTQTYICNVNHRKPSNTKVDPKSPKSCDKTHITCPCPAPELLGG	120	
QY	121	PSVFLPEPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNMYDGYEVNHNKTKPREEOYN	180	
DB	121	PSVFLPEPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNMYDGYEVNHNKTKPREEOYN	180	
QY	181	STYRVVSVLTFLHQWNNNGEKYKCVSNKALPAPLEKTISSKXVQPREQVYTLTPPSRDE	240	
DB	181	STYRVVSVLTFLHQWNNNGEKYKCVSNKALPAPLEKTISSKXVQPREQVYTLTPPSRDE	240	
QY	241	LTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPELVDPSGSPFLYSKLTVDKSRM	300	
DB	241	LTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPELVDPSGSPFLYSKLTVDKSRM	300	
QY	301	QCGNVFSCSVNHEALHNHYQOESLSLSPPCK	330	
DB	301	QCGNVFSCSVNHEALHNHYQOESLSLSPPCK	330	
RESULT 10				
ABR82103				
ID	ABR82103	standard; protein; 330 AA.		
XX	ABR82103;			
AC				
XX				
DT	23-SEP-2003	(first entry)		
XX				
DE		Human DR6 related amino acid sequence SEQ ID NO:5.		
XX				
KM		Human; DR6; B-cell mediated disease; immunosuppressive; antirheumatic;		
KM		antiarthritic; antisclerotic; dermatological; antiinflammatory;		
KM		antiproliferative; antidiabetic; cytostatic; neuroprotective; thyromimetic;		
KM		antitumor; nephrotoxic; antineoplastic; vasodilatory; vasopressin;		
KM		hepatocellular; antibacterial; antitumor; haemostatic; antianemic;		
XX		antimicrobial; anti-HIV; DR6 agonist; DR6 antagonist; immunity.		
OS		Homo sapiens.		
XX				
PN	WO2003051290-A2.			
PD				
XX	26-JUN-2003.			
PF				
XX	10-DEC-2002; 2002WO-US037596.			
XX				
PR	17-DEC-2001; 2001US-0342632P.			
XX				
PA	(ELIL ) LILLY & CO ELI.			
PI				
XX	Liu J, Na S, Song HY, Yang D;			
XX				
DR	WPI; 2003-541604/51.			
XX				
PT		Treating or preventing a B cell mediated condition e.g., chronic		
PT		hepatitis or chronic cirrhosis, in a mammal by administering a		
PT		pharmaceutical composition comprising a DR6 agonist or DR6 antagonist to		
XX		the mammal.		
PS				
XX		Disclosure; Page 96-97; 97p; English.		
CC				
CC		The present invention describes a method (M1) for treating or preventing		
CC		a B cell mediated condition in a mammal by administering a pharmaceutical		
CC		composition comprising a DR6 agonist or DR6 antagonist to the mammal.		
CC		Also described: (1) inhibiting B cell mediated immunity in a mammal, by		

Query Match	98.0% Score 1729	DB 6	Length 330
Best Local Similarity	97.9% Pred. No. 1.8e-122		
Matches 323	Conservative 3	Mismatches 4	Indels 0
			Gaps 0
QY	1	ASTGPGSVFPLABSSKSTSGCTALGCLVYDPPRPYTVSMNSGALTSGVHTPAVYQSS	60
DB	1	ASTGPGSVFPLABSSKSTSGCTALGCLVYDPPRPYTVSMNSGALTSGVHTPAVYQSS	60
QY	61	GLVLSLSSVWVWSSSLGTQYICVNNHKNKPSVTYDKDKVPEPSCKYTHCPPCAPPELLGG	120
DB	61	GLVLSLSSVWVWSSSLGTQYICVNNHKNKPSVTYDKDKVPEPSCKYTHCPPCAPPELLGG	120
QY	121	PSVFLPPKPKDPTLMISRTPEVTCVVDVSHEDPEVFNMYVDGVEVHANYKTKREBOYN	180
DB	121	PSVFLPPKPKDPTLMISRTPEVTCVVDVSHEDPEVFNMYVDGVEVHANYKTKREBOYN	180
QY	181	STRVVSVYLTLHDMNMWNGKAYKKCVSNKALPAIEKTTISKAKYQPREPOYTLTPERDE	240
DB	181	STRVVSVYLTLHDMNMWNGKAYKKCVSNKALPAIEKTTISKAKYQPREPOYTLTPERDE	240
QY	241	LTKQVSLTCLVKQFYPSPDIAVENESNGQPENNYKTPPVLYDSVGSFFLYSKLTVDSSRW	300
DB	241	LTKQVSLTCLVKQFYPSPDIAVENESNGQPENNYKTPPVLYDSVGSFFLYSKLTVDSSRW	300
QY	301	QQGNVFGSCVWHEALHNHYOQRSLSSPGK	330
DB	301	QQGNVFGSCVWHEALHNHYOQRSLSSPGK	330

RESULT 11

AA031102

```
ID      AA031102 standard; protein; 330 AA.
XX
AC      AA031102;
XX
DT      06-OCT-2003 (first entry)
XX
DE      Human A2-G8 scF antibody heavy chain constant region.
XX
KW      Human; antibody; stem cell factor; mast cell growth factor; asthma; scF;
XX      steel factor; c-kit ligand; gene therapy; heavy chain.
XX
OS      Homo sapiens.
XX
PN      WO2003051311-A2.
XX
PD      26-JUN-2003.
XX
PF      16-DEC-2002; 2002WO-US040227.
XX
PR      17-DEC-2001; 2001US-0342174P.
XX
PA      (FARB ) BAYER CORP.
XX
PI      Takeuchi T, Tomkinson A, Neben S;
XX      WPI; 2003-523500/49.
XX      N-PSDB; AAL62618.
XX
PT      New purified human antibody that binds to stem cell factor protein,
XX      useful for preparing a composition for treating asthma.
XX
PS      Example 10; Page 47-48; 94pp; English.
XX
SC      The invention provides human antibodies that bind to stem cell factor
XX      (SCF) protein. SCF is also known as mast cell growth factor, steel factor
XX      or c-kit ligand. Antibodies of the invention are useful for preparing
XX      compositions for treating asthma. They are also used in gene therapy. The
XX      present sequence is human SCF antibody heavy chain constant region
XX
SQ      Sequence 330 AA;
XX
Query Match      98.0%; Score 1729; DB 6; Length 330;
Best Local Similarity 97.9%; Pred. No. 1.8e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
XX
QY      1 ASTKGPSVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHPFPAVLQSS 60
DB      1 ASTKGPSVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHPFPAVLQSS 60
XX
QY      61 GLYSLSVVTVVPSSSLGTOTYICNVNHRKPSNTKVDKKVEPKSCDKTHHTCPCPAPRLGG 120
DB      61 GLYSLSVVTVVPSSSLGTOTYICNVNHRKPSNTKVDKKVEPKSCDKTHHTCPCPAPRLGG 120
XX
QY      121 PSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNAKTKRPREQYN 180
DB      121 PSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNAKTKRPREQYN 180
XX
QY      181 STYRVVSVLTVLHQMNMNGKEYCKVSNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240
DB      181 STYRVVSVLTVLHQMNMNGKEYCKVSNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240
XX
QY      241 LTRKQVSLTCLVKGFPSPDIAVWESNNGQPENNYKTTTPVLDSGSPFLYSKLTVDKSRW 300
DB      241 LTRKQVSLTCLVKGFPSPDIAVWESNNGQPENNYKTTTPVLDSGSPFLYSKLTVDKSRW 300
XX
QY      301 QOGNVFSSGVMEHALHNHYQQRSLSPK 330
DB      301 QOGNVFSSGVMEHALHNHYQQRSLSPK 330
XX
RESULT 12
ABR55836
ID      ABR55836 standard; proteoin; 330 AA.
```

```
XX
AC      ABR55836;
XX
DT      02-SEP-2003 (first entry)
XX
DE      Anti-Ang-2 antibody IgG1 constant region.
XX
KW      Ang-2; angiotensin-2; anorectic; cyrostatic; antiarteriosclerotic;
XX      gynaecological; antiinflammatory; osteopathic; antiporiatic; cancer;
XX      angiogenesis; antibody; human.
XX
OS      Homo sapiens.
XX
PN      WO2003030833-A2.
XX
PD      17-APR-2003.
XX
PF      11-OCT-2002; 2002WO-US032613.
XX
PR      11-OCT-2001; 2001US-0328604P.
XX      10-OCT-2002; 2002US-00269805.
XX
PA      (AMGE-) AMGEN INC.
XX
PI      Oliner JD;
XX      WPI; 2003-504963/47.
XX
PT      New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful
XX      for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
XX      hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
XX
PS      Example 4; Page 96; 161pp; English.
XX
SC      The invention relates to a specific binding agent, which comprises at
XX      least one peptide selected from any of 62 peptides (ABR55769-830) or its
XX      fragment. The binding agents are antibodies that recognize and bind to
XX      angiotensin-2 (Ang-2). The specific binding agent, particularly the
XX      antibody, is useful for inhibiting undesired angiogenesis, treating
XX      cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
XX      2 activity, modulating vascular permeability or plasma leakage, or
XX      treating a disease (e.g. ocular neovascular disease, obesity,
XX      haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
XX      inflammatory disorders, atherosclerosis, endometriosis, neoplastic
XX      disease, bone-related disease, or psoriasis) in a mammal. The present
XX      sequence represents a human IgG1 constant region of an anti-Ang-2
XX      antibody
XX
SQ      Sequence 330 AA;
XX
Query Match      98.0%; Score 1729; DB 6; Length 330;
Best Local Similarity 97.9%; Pred. No. 1.8e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
XX
QY      1 ASTKGPSVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHPFPAVLQSS 60
DB      1 ASTKGPSVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHPFPAVLQSS 60
XX
QY      61 GLYSLSVVTVVPSSSLGTOTYICNVNHRKPSNTKVDKKVEPKSCDKTHHTCPCPAPRLGG 120
DB      61 GLYSLSVVTVVPSSSLGTOTYICNVNHRKPSNTKVDKKVEPKSCDKTHHTCPCPAPRLGG 120
XX
QY      121 PSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNAKTKRPREQYN 180
DB      121 PSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNAKTKRPREQYN 180
XX
QY      181 STYRVVSVLTVLHQMNMNGKEYCKVSNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240
DB      181 STYRVVSVLTVLHQMNMNGKEYCKVSNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240
XX
QY      241 LTRKQVSLTCLVKGFPSPDIAVWESNNGQPENNYKTTTPVLDSGSPFLYSKLTVDKSRW 300
DB      241 LTRKQVSLTCLVKGFPSPDIAVWESNNGQPENNYKTTTPVLDSGSPFLYSKLTVDKSRW 300
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QY 301 OQGNVFGSCVMEALHNHYOQSLSLSPGK 330  
DB 301 OQGNVFGSCVMEALHNHYOQSLSLSPGK 330

## RESULT 13

AAO30893  
ID AAO30893 standard; protein; 330 AA.

AAO30893;  
XX

DT 22-SEP-2003 (first entry)  
XX

DE Human immunoglobulin gamma (IgG) 1 constant region.  
XX

KW Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;  
XX gene therapy; immunoglobulin; Ig; human.

OS Homo sapiens.  
XX

PN WO2003048334-A2.  
XX

PD 12-JUN-2003.  
XX

PF 04-DEC-2002; 2002WO-US038780.  
XX

PR 04-DEC-2001; 2001US-037113P.  
XX

PR 12-APR-2002; 2002US-0371966P.  
XX

PA (EMDL-) EMD LEXIGEN RES CENT CORP.  
XX

PI GILLIES SD;  
XX

DR WPI; 2003-513757/48.  
XX

PT New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2  
PT moiety, useful for preparing a composition for treating cancer, viral  
PT infections or immune disorders.  
XX

PS Example 1; Page 51-53; 71pp; English.  
XX

CC The invention relates to cytokine fusion proteins with increased  
CC therapeutic index and methods for increasing the therapeutic index of  
CC such fusion proteins. The fusion protein comprises a non-interleukin-2  
CC (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a  
CC composition for treating cancer, viral infections or immune disorders.  
CC The fusion protein is also used in gene therapy. The present sequence is  
CC human immunoglobulin gamma (IgG) constant region. This sequence is used  
CC to illustrate the method of the invention  
XX

SO Sequence 330 AA;  
XX

Query Match 98.0%; Score 1729; DB 6; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.8e-122;

Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKPSVFPPLAPSSKSTSGTALGCLVKDYFPEPVYTVSNVSGALTSVHTFPAYLQSS 60  
DB 1 ASTKPSVFPPLAPSSKSTSGTALGCLVKDYFPEPVYTVSNVSGALTSVHTFPAYLQSS 60

QY 61 GLYSLSVTVTVSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDKTHTPCPCPAPLQGG 120  
DB 61 GLYSLSVTVTVSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDKTHTPCPCPAPLQGG 120

QY 121 PSEVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEFVNAVTKPRREQYN 180  
DB 121 PSEVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEFVNAVTKPRREQYN 180

QY 181 STYRVAVSLTVLHOMNMNKEYKCKSNKALPAPLIEKTIISKAKGQREPOVYVTLPPSRDE 240  
DB 181 STYRVAVSLTVLHOMNMNKEYKCKSNKALPAPLIEKTIISKAKGQREPOVYVTLPPSRDE 240

QY 241 LTRNOVSLTCLVKGFPSPDIAVWESNGOPENNYKTPPVLDSDGSEFLYSKLTVDKSRN 300  
DB 241 LTRNOVSLTCLVKGFPSPDIAVWESNGOPENNYKTPPVLDSDGSEFLYSKLTVDKSRN 300

QY 301 OQGNVFGSCVMEALHNHYOQSLSLSPGK 330  
DB 301 OQGNVFGSCVMEALHNHYOQSLSLSPGK 330

## RESULT 14

ADFL1389  
ID ADFL1389 standard; protein; 330 AA.

ADFL1389;  
XX

DT 12-FEB-2004 (first entry)  
XX

DE Anti-OPGL antibody heavy chain constant region SEQ ID NO:2.  
XX

KW human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;  
XX osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.  
XX

OS Homo sapiens.  
XX

PN WO2003086289-A2.  
XX

PD 23-OCT-2003.  
XX

PF 07-APR-2003; 2003WO-US010749.  
XX

PR 05-APR-2002; 2002US-0370407P.  
XX

PA (AMGE-) AMGEN INC.  
XX

PI Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;  
XX

DR WPI; 2003-845253/78.  
XX

DR N-PSDB; ADFL1388.  
XX

PT New isolated antibody that specifically binds osteoprotegerin ligand,  
PT useful for diagnosing or treating bone disorders, such as osteoporosis,  
PT bone loss from arthritis, Paget's disease or osteopenia.  
XX

PS Example 3; SEQ ID NO 2; 156pp; English.  
XX

CC The present invention describes an isolated human antibody (1) that  
CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a  
CC pharmaceutical composition comprising a pharmaceutical carrier and a  
CC therapeutic amount of (1); (2) methods of treating an osteopenic disorder  
CC in a patient, comprising administering to a patient the pharmaceutical  
CC composition of (1) or a pharmaceutical amount of (1); and (3) a method  
CC for detecting OPGL in a biological sample, comprising contacting the  
CC sample with (1) under conditions that allow for binding of the antibody  
CC to OPGL, and measuring the level of bound antibody in the sample. (1) has  
CC osteopathic, antiarthritic and cytoskeletal activities, and can be used in  
CC gene therapy. The composition and methods are useful in diagnosing or  
CC treating bone disorders, such as osteoporosis, bone loss from arthritis,  
CC Paget's disease or osteopenia. The antibody (1) may also be used for  
CC detecting OPGL in biological samples and in identifying cells or tissues  
CC that produce the protein. The present sequence represents a sequence  
CC which is used in the exemplification of the present invention.  
XX

SO Sequence 330 AA;  
XX

Query Match 98.0%; Score 1729; DB 7; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.8e-122;

Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKPSVFPPLAPSSKSTSGTALGCLVKDYFPEPVYTVSNVSGALTSVHTFPAYLQSS 60  
DB 1 ASTKPSVFPPLAPSSKSTSGTALGCLVKDYFPEPVYTVSNVSGALTSVHTFPAYLQSS 60

QY 61 GLYSLSVVTVPSSSLGQTQYICNVNHNKPSNTKVDKVEPKSCDKTHPCPCPAPELLGG 120  
DB 61 GLYSLSVVTVPSSSLGQTQYICNVNHNKPSNTKVDKVEPKSCDKTHPCPCPAPELLGG 120  
QY 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFMVYDGYEVHNVKTKPREEQYN 180  
DB 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFMVYDGYEVHNVKTKPREEQYN 180  
QY 181 STYRVSVLTVLHQWMNGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240  
DB 181 STYRVSVLTVLHQWMNGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240  
QY 241 LTKNOVSLTCLVKGYPPSDIAVEMESNGQPENNYKTTTPVLDVSGSFPLYSKLTVDKSRM 300  
DB 241 LTKNOVSLTCLVKGYPPSDIAVEMESNGQPENNYKTTTPVLDVSGSFPLYSKLTVDKSRM 300  
QY 301 QQGNVFSCSVNHEALHNHYQKSLSPGK 330  
DB 301 QQGNVFSCSVNHEALHNHYQKSLSPGK 330

## RESULT 15

ADE97351  
ID ADE97351 standard; protein; 330 AA.

AC ADE97351;

DT 12-FEB-2004 (first entry)

DE Human IgG1 heavy chain constant region protein - SEQ ID 20.

XX immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin;  
KW virucide; antibacterial; anthrax; rhinovirus infection; common cold;  
KW intercellular adhesion molecule; ICAM-1; human; constant region; IgG.

OS Homo sapiens.

XX MO2003064992-A2.

XX 07-AUG-2003.

XX 25-OCT-2002; 2002MO-US034197.

XX 26-OCT-2001; 2001US-00047542.

XX (PLAN-) PLANET BIOTECHNOLOGY INC.

XX (LARRICK) LARRICK J W.

XX (WYCOFF) WYCOFF K L.

XX Larrick JW, Wycoff KL;

XX WPI; 2003-636816/60.

XX N-PSDB; ADE97350, ADE97376.

XX New immunoadhesin, useful for treating anthrax and rhinovirus, comprises

XX chimeric toxin receptor protein linked to immunoglobulin heavy chain, and

XX J chain and secretory component associated with the chimeric toxin

XX receptor protein.

XX Disclosure; SEQ ID NO 20; 288bp; English.

XX The invention relates to a novel immunoadhesin comprising a chimeric  
CC toxin receptor protein consisting of a toxin receptor protein linked to  
CC at least a portion of an immunoglobulin heavy chain with a J (joining)  
CC chain and secretory component (SC) associated with the chimeric toxin  
CC receptor protein. The immunoadhesin comprises a chimeric bacterial or  
CC viral toxin receptor protein and the immunoadhesin has plant-specific  
CC glycosylation. The immunoadhesin of the invention demonstrates virucide  
CC and antibacterial activities and may be useful for reducing the binding  
CC of a viral or bacterial antigen to a host cell and thus for treating or  
CC preventing anthrax, as well as human rhinovirus infection which results  
CC in the common cold. The current sequence is that of the human  
CC immunoadhesin-related protein of the invention.

XX SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 7; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSPVPLAPSSKSTSGTALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVLQSS 60  
DB 1 ASTKGPSPVPLAPSSKSTSGTALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVLQSS 60  
QY 61 GLYSLSVVTVPSSSLGQTQYICNVNHNKPSNTKVDKVEPKSCDKTHPCPCPAPELLGG 120  
DB 61 GLYSLSVVTVPSSSLGQTQYICNVNHNKPSNTKVDKVEPKSCDKTHPCPCPAPELLGG 120  
QY 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFMVYDGYEVHNVKTKPREEQYN 180  
DB 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFMVYDGYEVHNVKTKPREEQYN 180  
QY 181 STYRVSVLTVLHQWMNGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240  
DB 181 STYRVSVLTVLHQWMNGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240  
QY 241 LTKNOVSLTCLVKGYPPSDIAVEMESNGQPENNYKTTTPVLDVSGSFPLYSKLTVDKSRM 300  
DB 241 LTKNOVSLTCLVKGYPPSDIAVEMESNGQPENNYKTTTPVLDVSGSFPLYSKLTVDKSRM 300  
QY 301 QQGNVFSCSVNHEALHNHYQKSLSPGK 330  
DB 301 QQGNVFSCSVNHEALHNHYQKSLSPGK 330

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Job time : 172.565 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 09:01:44 ; Search time 144.767 Seconds

(without alignments)  
821.093 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 1599520

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1764	100.0	330	10	US-09-847-208-2
2	1764	100.0	330	10	US-10-000-439-2
3	1729	98.0	330	10	US-09-995-898A-15
4	1729	98.0	330	10	US-09-892-949-38
5	1729	98.0	330	13	US-10-047-542-20
6	1729	98.0	330	14	US-10-269-805-68
7	1729	98.0	330	14	US-10-310-719-8
8	1729	98.0	330	14	US-10-112-583-1
9	1729	98.0	330	14	US-10-320-231A-81
10	1729	98.0	330	15	US-10-383-902A-6
11	1729	98.0	330	15	US-10-408-901-2
12	1729	98.0	330	15	US-10-420-034A-15

13	1729	98.0	330	15	US-10-257-907-5	Sequence 5, Appli
14	1729	98.0	330	15	US-10-656-769-2	Sequence 2, Appli
15	1729	98.0	330	16	US-10-772-531-38	Sequence 38, Appli
16	1729	98.0	330	16	US-10-479-326-1	Sequence 1, Appli
17	1729	98.0	330	16	US-10-815-449-8	Sequence 8, Appli
18	1729	98.0	332	10	US-09-990-586-98	Sequence 98, Appli
19	1729	98.0	332	14	US-10-310-113-167	Sequence 167, App
20	1729	98.0	332	14	US-10-230-880-98	Sequence 98, Appli
21	1729	98.0	333	15	US-10-272-899A-8	Sequence 8, Appli
22	1729	98.0	356	15	US-10-272-899A-72	Sequence 72, Appli
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24	1729	98.0	371	14	US-10-097-044A-7	Sequence 7, Appli
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42	1729	98.0	446	15	US-10-435-229-7	Sequence 7, Appli
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45	1729	98.0	449	16	US-10-635-908-16	Sequence 16, Appli

#### ALIGNMENTS

RESULT 1

US-09-847-208-2

Sequence 2, Application US/09847208

Publication No. US20030082190A1

GENERAL INFORMATION:

APPLICANT: Saxon, Andrew

APPLICANT: Zhang, Ke

APPLICANT: Zhu, Daoceng

TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF

TITLE OF INVENTION: IGB-MEDIATED ALLERGIC DISEASES

FILE REFERENCE: UC67.002A

CURRENT APPLICATION NUMBER: US/09/847,208

CURRENT FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 177

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 330

TYPE: PRT

ORGANISM: Homo sapiens

US-09-847-208-2

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; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; FILE REFERENCE: UC067,004A
; CURRENT APPLICATION NUMBER: US/10/000,439
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 330
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; ORGANISM: Homo sapiens
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; Sequence 15, Application US/0995898A
; Publication No. US20030027253A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: No. US20030027253A1ak, Julia E.
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; APPLICANT: Whitmore, Theodore E.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
; FILE REFERENCE: 00-108
; CURRENT APPLICATION NUMBER: US/09/995,898A
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/253,561
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/267,211
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; ORGANISM: Homo sapiens
US-09-995-898A-15

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Best Local Similarity 97.9%; Pred. No. 5.9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPVFLPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60
Db 1 ASTKGPVFLPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
Db 61 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
Qy 121 PSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENHVKTKRPREOYN 180
Db 121 PSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENHVKTKRPREOYN 180
Qy 181 STYRVSVTLTVLHQMNMNGKEYCKVSNKALPAPIEKITSKAKVOPREQVYTLPPSRDE 240
Db 181 STYRVSVTLTVLHQMNMNGKEYCKVSNKALPAPIEKITSKAKVOPREQVYTLPPSRDE 240
Qy 241 LTKNOVSLTCLVKGFPSPDIAVWESNNGOPENNYYKTTTPVLDSVGSFFLYSKLTVDKSRW 300
Db 241 LTKNOVSLTCLVKGFPSPDIAVWESNNGOPENNYYKTTTPVLDSVGSFFLYSKLTVDKSRW 300
Qy 301 OQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
Db 301 OQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 4
US-09-892-949-38
; Sequence 38, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Geo, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuljper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 330
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-892-949-38

Query Match      98.0%; Score 1729; DB 10; Length 330;
Best Local Similarity 97.9%; Pred. No. 5 9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSPVEPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSVHTFPAVLQSS 60
DB 1 ASTKGPSPVEPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSVHTFPAVLQSS 60
QY 61 GLYSLSSTVTVSSSLGTQTYICNNVHKSNKVDKKVPEPKSCDKHTHTCPCPAPPELLGG 120
DB 61 GLYSLSSTVTVSSSLGTQTYICNNVHKSNKVDKKVPEPKSCDKHTHTCPCPAPPELLGG 120
QY 121 PSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVVHNAKTKPRREQYN 180
DB 121 PSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVVHNAKTKPRREQYN 180
QY 181 STYRVSVLTVLHQWMNNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQWMNNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
QY 241 LTRKQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 241 LTRKQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 OQGNVFSCSVMEHALHNHYQORSLSLSPGK 330
DB 301 OQGNVFSCSVMEHALHNHYQORSLSLSPGK 330

RESULT 5
US-10-047-542-20
; Sequence 20, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARICK, JAMES W.
; APPLICANT: MYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.C1P1
; CURRENT APPLICATION NUMBER: US/10/047,542
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 20
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-20

Query Match      98.0%; Score 1729; DB 13; Length 330;
Best Local Similarity 97.9%; Pred. No. 5 9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSPVEPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSVHTFPAVLQSS 60
DB 1 ASTKGPSPVEPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSVHTFPAVLQSS 60
QY 61 GLYSLSSTVTVSSSLGTQTYICNNVHKSNKVDKKVPEPKSCDKHTHTCPCPAPPELLGG 120
DB 61 GLYSLSSTVTVSSSLGTQTYICNNVHKSNKVDKKVPEPKSCDKHTHTCPCPAPPELLGG 120
QY 121 PSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVVHNAKTKPRREQYN 180
DB 121 PSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVVHNAKTKPRREQYN 180
QY 181 STYRVSVLTVLHQWMNNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQWMNNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
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DB 181 STYRVSVLTVLHQWMNNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
QY 241 LTRKQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 241 LTRKQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 OQGNVFSCSVMEHALHNHYQORSLSLSPGK 330
DB 301 OQGNVFSCSVMEHALHNHYQORSLSLSPGK 330

RESULT 6
US-10-269-805-68
; Sequence 68, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 68
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-68

Query Match      98.0%; Score 1729; DB 14; Length 330;
Best Local Similarity 97.9%; Pred. No. 5 9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSPVEPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSVHTFPAVLQSS 60
DB 1 ASTKGPSPVEPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSVHTFPAVLQSS 60
QY 61 GLYSLSSTVTVSSSLGTQTYICNNVHKSNKVDKKVPEPKSCDKHTHTCPCPAPPELLGG 120
DB 61 GLYSLSSTVTVSSSLGTQTYICNNVHKSNKVDKKVPEPKSCDKHTHTCPCPAPPELLGG 120
QY 121 PSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVVHNAKTKPRREQYN 180
DB 121 PSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVVHNAKTKPRREQYN 180
QY 181 STYRVSVLTVLHQWMNNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQWMNNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
QY 241 LTRKQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 241 LTRKQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 OQGNVFSCSVMEHALHNHYQORSLSLSPGK 330
DB 301 OQGNVFSCSVMEHALHNHYQORSLSLSPGK 330
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|||||:|||||
US-10-310-719-8
; Sequence 8, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: Lex-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04

RESULT 7
US-10-310-719-8
; Sequence 8, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: Lex-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
```

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; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc
; LOCATION: (1)..(330)
; OTHER INFORMATION: IgG1 constant region
US-10-310-719-8

Query Match          98.0%; Score 1729; DB 14; Length 330;
Best Local Similarity 97.9%; Pred. No. 5.9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNVSGALTSGLTHFPAPVLAQSS 60
DB 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNVSGALTSGLTHFPAPVLAQSS 60

QY 61 GLYSLSVVTVPSSSLGTQTYICNNVHKPSNTKVDKKEPKSCDKTHPCPCPAPPELLGG 120
DB 61 GLYSLSVVTVPSSSLGTQTYICNNVHKPSNTKVDKKEPKSCDKTHPCPCPAPPELLGG 120

QY 121 PSVFLPPEPKKDTLMISRTPEVTCVVDVSHEDPEVKFMVYDGVGVNNAKTKPREEOYN 180
DB 121 PSVFLPPEPKKDTLMISRTPEVTCVVDVSHEDPEVKFMVYDGVGVNNAKTKPREEOYN 180

QY 181 STYRVVSVLTVLHQWMNNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
DB 181 STYRVVSVLTVLHQWMNNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240

QY 241 LTRKNQVSLTCLVKGYFSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTIVDKSRW 300
DB 241 LTRKNQVSLTCLVKGYFSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTIVDKSRW 300

QY 301 QOQNVFSCSVHMEALHNHYOQRSLSLSPGK 330
DB 301 QOQNVFSCSVHMEALHNHYOQRSLSLSPGK 330

RESULT 8
US-10-112-582-1
; Sequence 1, Application US/10112582
; Publication No. US2003016687A1
; GENERAL INFORMATION:
; APPLICANT: Glilies, Stephen
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
; FILE REFERENCE: LEX-017
; CURRENT APPLICATION NUMBER: US/10/112,582
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/280,625
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc
; OTHER INFORMATION: human Ig gamma heavy chain C region
US-10-112-582-1

Query Match          98.0%; Score 1729; DB 14; Length 330;
Best Local Similarity 97.9%; Pred. No. 5.9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNVSGALTSGLTHFPAPVLAQSS 60
DB 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNVSGALTSGLTHFPAPVLAQSS 60
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QY 61 GLYSLSVVTVPSSSLGTQTYICNNVHKPSNTKVDKKEPKSCDKTHPCPCPAPPELLGG 120
DB 61 GLYSLSVVTVPSSSLGTQTYICNNVHKPSNTKVDKKEPKSCDKTHPCPCPAPPELLGG 120

QY 121 PSVFLPPEPKKDTLMISRTPEVTCVVDVSHEDPEVKFMVYDGVGVNNAKTKPREEOYN 180
DB 121 PSVFLPPEPKKDTLMISRTPEVTCVVDVSHEDPEVKFMVYDGVGVNNAKTKPREEOYN 180

QY 181 STYRVVSVLTVLHQWMNNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
DB 181 STYRVVSVLTVLHQWMNNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240

QY 241 LTRKNQVSLTCLVKGYFSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTIVDKSRW 300
DB 241 LTRKNQVSLTCLVKGYFSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTIVDKSRW 300

QY 301 QOQNVFSCSVHMEALHNHYOQRSLSLSPGK 330
DB 301 QOQNVFSCSVHMEALHNHYOQRSLSLSPGK 330
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RESULT 9
US-10-320-231A-81
; Sequence 81, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 81
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-320-231A-81
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Query Match          98.0%; Score 1729; DB 14; Length 330;
Best Local Similarity 97.9%; Pred. No. 5.9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNVSGALTSGLTHFPAPVLAQSS 60
DB 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNVSGALTSGLTHFPAPVLAQSS 60

QY 61 GLYSLSVVTVPSSSLGTQTYICNNVHKPSNTKVDKKEPKSCDKTHPCPCPAPPELLGG 120
DB 61 GLYSLSVVTVPSSSLGTQTYICNNVHKPSNTKVDKKEPKSCDKTHPCPCPAPPELLGG 120

QY 121 PSVFLPPEPKKDTLMISRTPEVTCVVDVSHEDPEVKFMVYDGVGVNNAKTKPREEOYN 180
DB 121 PSVFLPPEPKKDTLMISRTPEVTCVVDVSHEDPEVKFMVYDGVGVNNAKTKPREEOYN 180

QY 181 STYRVVSVLTVLHQWMNNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
DB 181 STYRVVSVLTVLHQWMNNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240

QY 241 LTRKNQVSLTCLVKGYFSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTIVDKSRW 300
DB 241 LTRKNQVSLTCLVKGYFSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTIVDKSRW 300

QY 301 QOQNVFSCSVHMEALHNHYOQRSLSLSPGK 330
DB 301 QOQNVFSCSVHMEALHNHYOQRSLSLSPGK 330
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Db 121 PSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGEVHNAAKTKPREEQYN 180
Qy 181 STYRVSVLTVLHQWMNGKEYCKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQWMNGKEYCKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Qy 241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNNYKTTTPVLDVSGSFILYSLKLTVDKSRW 300
Db 241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNNYKTTTPVLDVSGSFILYSLKLTVDKSRW 300
Qy 301 QCGNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 301 QCGNVFSCSVMEALHNHYTQKSLSLSPGK 330

RESULT 13
US-10-257-907-5
; Sequence 5, Application US/10257907
; Publication No. US20040043022A1
; GENERAL INFORMATION:
; APPLICANT: Heuer, Josef
; APPLICANT: Liu, Jingqi
; APPLICANT: Na, Songqing
; APPLICANT: Song, Ho Yeong
; APPLICANT: Yang, Derek Di
; TITLE OF INVENTION: TREATING T-CELL MEDIATED DISEASES BY MODULATING DR6 ACTIVITY
; FILE REFERENCE: X-131992
; CURRENT APPLICATION NUMBER: US/10/257,907
; CURRENT FILING DATE: 2002-10-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-907-5

Query Match 98.0%; Score 1729; DB 15; Length 330;
Best Local Similarity 97.9%; Pred. No. 5,9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPVPEPLAPSSKSTSGGTALGCLVKDYFPEPTVSNMSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPVPEPLAPSSKSTSGGTALGCLVKDYFPEPTVSNMSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
Db 61 GLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
Qy 121 PSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGEVHNAAKTKPREEQYN 180
Db 121 PSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGEVHNAAKTKPREEQYN 180
Qy 181 STYRVSVLTVLHQWMNGKEYCKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQWMNGKEYCKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Qy 241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNNYKTTTPVLDVSGSFILYSLKLTVDKSRW 300
Db 241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNNYKTTTPVLDVSGSFILYSLKLTVDKSRW 300
Qy 301 QCGNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 301 QCGNVFSCSVMEALHNHYTQKSLSLSPGK 330

RESULT 14
US-10-656-769-2
; Sequence 2, Application US/10656769
; Publication No. US20040097712A1
; GENERAL INFORMATION:
; APPLICANT: Varnum, Brian
```

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; APPLICANT: Witte, Allison
; APPLICANT: Wezina, Chris
; APPLICANT: Wong, Lu Min
; APPLICANT: Qian, Xueming
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
; FILE REFERENCE: 01,1554
; CURRENT APPLICATION NUMBER: US/10/656,769
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-2

Query Match 98.0%; Score 1729; DB 15; Length 330;
Best Local Similarity 97.9%; Pred. No. 5,9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPVPEPLAPSSKSTSGGTALGCLVKDYFPEPTVSNMSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPVPEPLAPSSKSTSGGTALGCLVKDYFPEPTVSNMSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
Db 61 GLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
Qy 121 PSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGEVHNAAKTKPREEQYN 180
Db 121 PSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGEVHNAAKTKPREEQYN 180
Qy 181 STYRVSVLTVLHQWMNGKEYCKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQWMNGKEYCKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Qy 241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNNYKTTTPVLDVSGSFILYSLKLTVDKSRW 300
Db 241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNNYKTTTPVLDVSGSFILYSLKLTVDKSRW 300
Qy 301 QCGNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 301 QCGNVFSCSVMEALHNHYTQKSLSLSPGK 330

RESULT 15
US-10-772-531-38
; Sequence 38, Application US/10772531
; Publication No. US20040142422A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/10/772,531
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 330
; TYPE: PRT
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ORGANISM: Homo sapiens  
US-10-772-531-38

Query Match 98.0%; Score 1729; DB 16; Length 330;  
Best Local Similarity 97.9%; Pred. No. 5, 9e-126;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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QY 1 ASTKGSPVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGSPVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSTVTVPSSTSLGTOTYICNVNHNKSNNTKVDKKVPEPKSCDKTHTCPPCPAPELLGG 120
DB 61 GLYSLSSTVTVPSSTSLGTOTYICNVNHNKSNNTKVDKKVPEPKSCDKTHTCPPCPAPELLGG 120
QY 121 PSVFLEPPPKDITLMTSRTPEVTGVVDVSHEDPEYKFNMYVDGVEVHNKTKPREEOYN 180
DB 121 PSVFLEPPPKDITLMTSRTPEVTGVVDVSHEDPEYKFNMYVDGVEVHNKTKPREEOYN 180
QY 181 STYRVVSVLTVLHQMMNGKEYKCKVSNKALPAPIEKTI SKAKVQPREPOVYTLPPSRDE 240
DB 181 STYRVVSVLTVLHQMMNGKEYKCKVSNKALPAPIEKTI SKAKVQPREPOVYTLPPSRDE 240
QY 241 LTRKQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300
DB 241 LTRKQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSQVMHEALHNHYQQRSLSLSPGK 330
DB 301 QQGNVFSQVMHEALHNHYQQRSLSLSPGK 330
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Search completed: June 7, 2005, 09:25:06  
Job time : 145.767 secs



**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 08:49:07 ; Search time 46.1658 Seconds  
(without alignments)  
533.603 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764

Sequence: 1 ASTKGPSVPLAPSSKSTSG.....MHEALHNHYQQRSLSPGK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA:\*  
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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
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6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1729	98.0	371	1	US-08-236-311-7
2	1729	98.0	371	3	US-08-457-918-7
3	1729	98.0	371	4	US-10-157-408-7
4	1729	98.0	446	3	US-08-397-411-7
5	1729	98.0	449	1	US-08-458-516-13
6	1729	98.0	467	4	US-08-030-175-41
7	1729	98.0	467	4	US-08-030-175-42
8	1729	98.0	476	2	US-08-378-939-10
9	1729	98.0	547	4	US-09-746-359A-54
10	1729	98.0	567	4	US-09-825-561A-16
11	1729	98.0	571	4	US-09-746-359B-53
12	1729	98.0	951	4	US-09-313-942-9
13	1725	97.8	462	4	US-09-289-942A-7
14	1725	97.8	476	3	US-09-740-002-27
15	1725	97.8	476	3	US-08-487-550-4
16	1725	97.8	476	3	US-08-487-550-12
17	1725	97.8	476	4	US-09-526-098-4
18	1725	97.8	476	4	US-09-526-098-12
19	1725	97.8	476	4	US-09-383-916-4
20	1725	97.8	476	4	US-09-383-916-12
21	1725	97.8	478	3	US-08-487-550-8
22	1725	97.8	478	4	US-09-526-098-8
23	1725	97.8	478	4	US-09-383-916-8
24	1724	97.7	459	1	US-08-157-101A-7
25	1724	97.7	475	4	US-09-740-002-25
26	1723	97.7	330	4	US-09-301-593-22
27	1723	97.7	451	2	US-08-887-352B-14

28	1723	97.7	451	2	US-08-887-352B-16	Sequence 16, Appl
29	1723	97.7	451	2	US-08-887-352B-18	Sequence 18, Appl
30	1723	97.7	451	3	US-08-466-151-65	Sequence 65, Appl
31	1723	97.7	451	3	US-09-109-207C-14	Sequence 14, Appl
32	1723	97.7	451	3	US-09-109-207C-16	Sequence 16, Appl
33	1723	97.7	451	3	US-09-109-207C-18	Sequence 18, Appl
34	1723	97.7	451	3	US-09-282-505-2	Sequence 2, Appl
35	1723	97.7	451	3	US-09-054-255-2	Sequence 2, Appl
36	1723	97.7	451	3	US-09-296-005-14	Sequence 14, Appl
37	1723	97.7	451	3	US-09-296-005-16	Sequence 16, Appl
38	1723	97.7	451	3	US-09-296-005-18	Sequence 18, Appl
39	1723	97.7	451	4	US-09-282-846-2	Sequence 2, Appl
40	1723	97.7	451	4	US-09-680-145-2	Sequence 2, Appl
41	1723	97.7	451	4	US-09-920-171-14	Sequence 14, Appl
42	1723	97.7	451	4	US-09-920-171-16	Sequence 16, Appl
43	1723	97.7	451	4	US-09-920-171-18	Sequence 18, Appl
44	1723	97.7	451	4	US-09-716-028-14	Sequence 14, Appl
45	1723	97.7	451	4	US-09-716-028-16	Sequence 16, Appl

#### ALIGNMENTS

RESULT 1  
US-08-236-311-7  
; Sequence 7, Application US/08236311  
; Patent No. 5565335  
; GENERAL INFORMATION:  
; APPLICANT: Capon, Daniel J.  
; APPLICANT: Gregory, Timothy J.  
; TITLE OF INVENTION: Adhesion Variants  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,311  
; FILING DATE: 02-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/936190  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/842777  
; FILING DATE: 18-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/250785  
; FILING DATE: 28-SEP-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/104329  
; FILING DATE: 02-OCT-1987  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 444PIC2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1996  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 371 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

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US-08-236-311-7
Query Match          98.0%; Score 1729; DB 1; Length 371;
Best Local Similarity 97.9%; Pred. No. 3.2e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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   |||
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   |||
QY 121 PSVFLFPPPKPDITLMSRTPPEVTCVVDVSHEDPEVKFNMVYDGEVHNKTKPREBOYN 180
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DB 162 PSVFLFPPPKPDITLMSRTPPEVTCVVDVSHEDPEVKFNMVYDGEVHNKTKPREBOYN 221
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QY 181 STYRVSVTLTVLHQWMNKGKEYCKVSNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240
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DB 222 STYRVSVTLTVLHQWMNKGKEYCKVSNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 281
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QY 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDVSQSFFLYSKLTVDKSRW 300
   |||
DB 282 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDVSQSFFLYSKLTVDKSRW 341
   |||
QY 301 QOQNVFSCSVMEALHNHYQORSLSLSPGK 330
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DB 342 QOQNVFSCSVMEALHNHYTOKSLSLSPGK 371
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RESULT 2
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Koblinc, Jeffrey S.
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REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444P1C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-457-918-7
Query Match          98.0%; Score 1729; DB 3; Length 371;
Best Local Similarity 97.9%; Pred. No. 3.2e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKPSVFPPLAPSSKSTSGGTAALGCLVKQYFPPRVTYSNMNSGALTSQVHFPFPAVLQSS 60
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DB 42 ASTKGPSPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVYVSNMNSGALTSQVHFPFPAVLQSS 101
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QY 61 GLYSLSVVTVPSSSLGQTQYICNVNHRKPSNTKVDKVEPKSCDKTHHTCPCPAPPELLGG 120
   |||
DB 102 GLYSLSVVTVPSSSLGQTQYICNVNHRKPSNTKVDKVEPKSCDKTHHTCPCPAPPELLGG 161
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QY 121 PSVFLFPPPKPDITLMSRTPPEVTCVVDVSHEDPEVKFNMVYDGEVHNKTKPREBOYN 180
   |||
DB 162 PSVFLFPPPKPDITLMSRTPPEVTCVVDVSHEDPEVKFNMVYDGEVHNKTKPREBOYN 221
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QY 181 STYRVSVTLTVLHQWMNKGKEYCKVSNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240
   |||
DB 222 STYRVSVTLTVLHQWMNKGKEYCKVSNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 281
   |||
QY 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDVSQSFFLYSKLTVDKSRW 300
   |||
DB 282 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDVSQSFFLYSKLTVDKSRW 341
   |||
QY 301 QOQNVFSCSVMEALHNHYQORSLSLSPGK 330
   |||
DB 342 QOQNVFSCSVMEALHNHYTOKSLSLSPGK 371
   |||

RESULT 3
US-10-157-408-7
; Sequence 7, Application US/10157408
; Patent No. 6710169
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/157,408
; FILING DATE: 28-May-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 07/936190
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FILED DATE: 26-AUG-1992  
APPLICATION NUMBER: 07/842777  
FILING DATE: 18-FEB-1992  
APPLICATION NUMBER: 07/250785  
FILING DATE: 28-SEP-1988  
APPLICATION NUMBER: 07/104329  
FILING DATE: 02-OCT-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubinec, Jeffrey S.  
REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0444PIC3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8228  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 371 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-157-408-7

Query Match 98.0%; Score 1729; DB 4; Length 371;  
Best Local Similarity 97.9%; Pred. No. 3.2e-157;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGSVPFLAPSSSKTSSTGGTALGCLVKDYFPEPVTVSNMGSALTSGVHFPAYLQSS 60  
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QY 61 GLYSLSVTVTVSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPPELLGG 120  
DB 102 GLYSLSVTVTVSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPPELLGG 161  
QY 121 PSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFMVYDGVVHNAKTKPREEOYN 180  
DB 162 PSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFMVYDGVVHNAKTKPREEOYN 221  
QY 181 STYRVSVTLTVLHQMNGKEKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240  
DB 222 STYRVSVTLTVLHQMNGKEKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 281  
QY 241 LTRNQVSLTCLVKGFYPSDIAVWESNQPENNYKTTIPVLDVSGSFFLYSKLTVDKSRW 300  
DB 282 LTRNQVSLTCLVKGFYPSDIAVWESNQPENNYKTTIPVLDVSGSFFLYSKLTVDKSRW 341  
QY 301 QOQNVFSCSVMEHALHNHYQORSLSLSPGK 330  
DB 342 QOQNVFSCSVMEHALHNHYQORSLSLSPGK 371

RESULT 4  
US-08-397-411-7  
Sequence 7, Application US/08397411  
Patent No. 6129914  
GENERAL INFORMATION:  
APPLICANT: Weiner, George  
APPLICANT: Gingrich, Roger  
APPLICANT: Link, Brian  
APPLICANT: Teo, J. Yun  
TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,411  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/859,583  
FILING DATE: 27-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-004901  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 446 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-397-411-7

Query Match 98.0%; Score 1729; DB 3; Length 446;  
Best Local Similarity 97.9%; Pred. No. 4.2e-157;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGSVPFLAPSSSKTSSTGGTALGCLVKDYFPEPVTVSNMGSALTSGVHFPAYLQSS 60  
DB 117 ASTKGSVPFLAPSSSKTSSTGGTALGCLVKDYFPEPVTVSNMGSALTSGVHFPAYLQSS 176  
QY 61 GLYSLSVTVTVSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPPELLGG 120  
DB 177 GLYSLSVTVTVSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPPELLGG 236  
QY 121 PSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFMVYDGVVHNAKTKPREEOYN 180  
DB 237 PSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFMVYDGVVHNAKTKPREEOYN 296  
QY 181 STYRVSVTLTVLHQMNGKEKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240  
DB 297 STYRVSVTLTVLHQMNGKEKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 356  
QY 241 LTRNQVSLTCLVKGFYPSDIAVWESNQPENNYKTTIPVLDVSGSFFLYSKLTVDKSRW 300  
DB 357 LTRNQVSLTCLVKGFYPSDIAVWESNQPENNYKTTIPVLDVSGSFFLYSKLTVDKSRW 416  
QY 301 QOQNVFSCSVMEHALHNHYQORSLSLSPGK 330  
DB 417 QOQNVFSCSVMEHALHNHYQORSLSLSPGK 446

RESULT 5  
US-08-458-516-13  
Sequence 13, Application US/08458516  
Patent No. 5777085  
GENERAL INFORMATION:  
APPLICANT: Co, Man Sung  
APPLICANT: Teo, J. Yun  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
TITLE OF INVENTION: GRIB/IIIIA  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

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Query Match	98.0%;	Score 1729;	DB 1;	Length 449;
Best Local Similarity	97.9%;	Pred. No. 4.3e-157;		
Matches 323; Conservative	3;	Mismatches 4;	Indels 0;	Gaps 0

QY	1	ASTGSPSVFPLAPBSKSTSGGTALGCLVCKVYFPPPVYVSNMGSALTSGVHFFPAVLQSS	60
Db	120	ASTGSPSVFPLAPBSKSTSGGTALGCLVCKVYFPPPVYVSNMGSALTSGVHFFPAVLQSS	179
QY	61	GLYSLSVYVYVYVSSSLGTQTYI CVNNHKKPSNTKDXKAPKSCDKTHTCPCPABELLGG	120
Db	180	GLYLSLSVYVYVYVSSSLGTQTYI CVNNHKKPSNTKDXKAPKSCDKTHTCPCPABELLGG	239
QY	121	PSVELFPKPCKDTLMI SRTPEVTCVYVDSHEDPEVKENMYVDGEVHNKTKPREEOYN	180
Db	240	PSVFLFPKPCKDTLMI SRTPEVTCVYVDSHEDPEVKENMYVDGEVHNKTKPREEOYN	299
QY	181	STYVYVSVLTVLHQNMMNGKEYCKCNKALPAPLEKTIISAKXVOPREOVYTLPPSDE	240
Db	300	STYVYVSVLTVLHQNMMNGKEYCKCNKALPAPLEKTIISAKXGPREOVYTLPPSDE	359
QY	241	LTKQVSLTCLVKGFPSPDI AVEWESNQPENNYKTPTPVLVDSVGSFFLYSKLTVDKSRM	300
Db	360	LTKQVSLTCLVKGFPSPDI AVEWESNQPENNYKTPTPVLVDSVGSFFLYSKLTVDKSRM	419
QY	301	QQGNVFSQVNHLEALHNHYOQRSLSTSPGK	330
Db	420	QQGNVFSQVNHLEALHNHYOQRSLSTSPGK	449

RESULT 6  
US-08-030-175-41  
Sequence 41, Application US/08030175  
Patent No. 6767996  
GENERAL INFORMATION:  
APPLICANT: Gorman, Scott D.  
APPLICANT: Clark, Michael R.  
APPLICANT: Cobbold, Stephen P.  
APPLICANT: Waldmann, Herman  
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.  
STREET: 555 13TH ST., NW Suite 701 East  
CITY: Washington  
STATE: D. C.  
COUNTRY: U.S.

```

ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage
COMPUTER: IBM AT compatible
OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
SOFTWARE: WordPerfect 5.0 (Dos Text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,175
FILING DATE: 17-MAY-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01578
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1768-113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
OS-08-030-175-41

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Query Match	98.0%;	Score 1729;	DB 4;	length 467;
Best Local Similarity	97.9%;	Pred. No. 4.5e-157;		
Matches 323; Conservative	3;	Mismatches 4;	Indels 0;	Gaps 0;

QY	1	ASRKGVEPFPLAASKSSTSGTALGCLVNDYFPEPLTVSNNSGALTSGVHTPPAVLQSS	60
QY	138	ASTKGPVFPFLABSSKSTSGTALGCLVNDYFPEPLTVSNNSGALTSGVHTPPAVLQSS	197
QY	61	GLYSLSVVWVPSSSLGTQTYI CAVNAHKPSNTKYDKKVEPKSCDKHTKCPCPAPELLGG	120
Db	198	GLYSLSVVWVPSSSLGTQTYI CAVNAHKPSNTKYDKKVEPKSCDKHTKCPCPAPELLGG	257
QY	121	PSVFLPFPKPKDQTLMTSRTEPVTCVVVDVSHEDDEVKFNMYVDGVEVHNVKTKPREEQYN	180
Db	258	PSVFLPFPKPKDQTLMTSRTEPVTCVVVDVSHEDDEVKFNMYVDGVEVHNVKTKPREEQYN	317
QY	181	STTRVSVLTVLHONMMNGKRYCKCKVSNKALPAIEKTIISAKYQPREPQYITLPPSDE	240
Db	318	STTRVSVLTVLHONMMNGKRYCKCKVSNKALPAIEKTIISAKYQPREPQYITLPPSDE	377
QY	241	LTKNQVSLTCLVNGFYPSDIAVENHSNQGPENNNKTTTPVLDVSGSFPLYEKLTVDKSRW	300
Db	378	LTKNQVSLTCLVNGFYPSDIAVENHSNQGPENNNKTTTPVLDVSGSFPLYEKLTVDKSRW	437
QY	301	QGGNVFSCSVMEALHNHYQORSLSLSPGK	330
Db	438	QGGNVFSCSVMEALHNHYQORSLSLSPGK	467

RESULT 7  
US-08-030-175-42  
Sequence 42, Application US/08030175  
Patent No. 6767996  
GENERAL INFORMATION:  
APPLICANT: Gorman, Scott D.  
APPLICANT: Clark, Michael R.  
APPLICANT: Cobbold, Stephen P.  
APPLICANT: Waldmann, Herman  
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.  
STREET: 555 13TH ST., NW Suite 701 East  
CITY: Washington  
STATE: D. C.

COUNTRY: U.S.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage  
COMPUTER: IBM AT compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2  
SOFTWARE: Wordperfect 5.0 (dos text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/030,175  
FILING DATE: 17-MAY-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB91/01578  
FILING DATE: 13-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Ernst, Barbara G.  
REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1768-113  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)783-6040  
TELEFAX: (202)783-6031  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-030-175-42

Query Match 98.0%; Score 1729; DB 4; Length 467;  
Best Local Similarity 97.9%; Pred. No. 4.5e-157;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
1 ASTKGSVPFLPSSKSTSGTAAAGCLVKDYFPEPVYTMNMSGALTSVHTFPAVLQSS 60  
138 ASTKGSVPFLPSSKSTSGTAAAGCLVKDYFPEPVYTMNMSGALTSVHTFPAVLQSS 197  
61 GLYSLSVTVVSSSSIGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPPELLGG 120  
198 GLYSLSVTVVSSSSIGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPPELLGG 257  
121 PSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVVHNHAKTKPREEOYN 180  
258 PSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVVHNHAKTKPREEOYN 317  
181 STYRVSVTLVHQMNNKEKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240  
338 STYRVSVTLVHQMNNKEKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 377  
241 LTRKQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRM 300  
376 LTRKQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRM 437  
QY 301 OQGNVFSCVMHEALHNHYQORSLSLSPGK 330  
DB 438 OQGNVFSCVMHEALHNHYQORSLSLSPGK 467

RESULT 8  
US-08-378-939-10  
Sequence 10, Application US/08378939  
Patent No. 5876961  
GENERAL INFORMATION:  
APPLICANT: CROME, JAMES SCOTT  
APPLICANT: LEWIS, ALAN PETER  
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: ROTHWELL, FIGG, ERNST & KURZ  
STREET: 555 THIRTEENTH ST. N.W.  
CITY: WASHINGTON  
STATE: D. C.  
COUNTRY: U.S.

ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,939  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/952640  
FILING DATE: 01-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: ERNST, BARBARA G.  
REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1808-118  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-378-939-10

Query Match 98.0%; Score 1729; DB 2; Length 476;  
Best Local Similarity 97.9%; Pred. No. 4.7e-157;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
1 ASTKGSVPFLPSSKSTSGTAAAGCLVKDYFPEPVYTMNMSGALTSVHTFPAVLQSS 60  
147 ASTKGSVPFLPSSKSTSGTAAAGCLVKDYFPEPVYTMNMSGALTSVHTFPAVLQSS 206  
61 GLYSLSVTVVSSSSIGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPPELLGG 120  
207 GLYSLSVTVVSSSSIGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPPELLGG 266  
121 PSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVVHNHAKTKPREEOYN 180  
267 PSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVVHNHAKTKPREEOYN 326  
181 STYRVSVTLVHQMNNKEKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240  
327 STYRVSVTLVHQMNNKEKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 386  
241 LTRKQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRM 300  
387 LTRKQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRM 446  
QY 301 OQGNVFSCVMHEALHNHYQORSLSLSPGK 330  
DB 447 OQGNVFSCVMHEALHNHYQORSLSLSPGK 476

RESULT 9  
US-09-746-359A-54  
Sequence 54, Application US/09746359A  
Patent No. 6610286  
GENERAL INFORMATION:  
APPLICANT: Thompson, Penny  
APPLICANT: Foster, Donald C.  
APPLICANT: Xu, Wenfeng  
APPLICANT: Madden, Karen L.  
APPLICANT: Kelly, James D.  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Blumberg, Hal  
APPLICANT: Eagan, Maribeth A.  
APPLICANT: Jaspers, Stephen R.  
APPLICANT: Chandrasekhar, Yamin A.  
APPLICANT: No. 6610286ak, Julia E.

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; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-746-359A-54

Query Match          98.0%; Score 1729; DB 4; Length 547;
Best Local Similarity 97.9%; Pred. No. 5,7e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1  ASTGPPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMNSGALTSGVHTFPAVLQSS 60
DB      218  ASTGPPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMNSGALTSGVHTFPAVLQSS 277
QY      61  GLYSLSVVTVPSSSLGTQTYICNNHKSNTKVDKVEPKSCDKTHTCPCPAPABELLG 120
DB      278  GLYSLSVVTVPSSSLGTQTYICNNHKSNTKVDKVEPKSCDKTHTCPCPAPABELLG 337
QY      121  PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAKTRPREEOYN 180
DB      338  PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAKTRPREEOYN 397
QY      181  STYRVSVLTVLHQMWNNGKEYCKVSNKALPAPIEKTIISKAKQPREPOVYTLPPSRDE 240
DB      398  STYRVSVLTVLHQMWNNGKEYCKVSNKALPAPIEKTIISKAKQPREPOVYTLPPSRDE 457
QY      241  LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
DB      458  LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 517
QY      301  QOGNVFSCSVMEALAHNHYQORSLSLSPGK 330
DB      518  QOGNVFSCSVMEALAHNHYQORSLSLSPGK 547

RESULT 10
US-09-825-561A-16
; Sequence 16, Application US/09825561A
; Patent No. 6777539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 6777539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: soluble zalphai1R/IgGgamma1 polypeptide
US-09-825-561A-16
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Query Match          98.0%; Score 1729; DB 4; Length 567;
Best Local Similarity 97.9%; Pred. No. 6.1e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1  ASTGPPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMNSGALTSGVHTFPAVLQSS 60
DB      238  ASTGPPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMNSGALTSGVHTFPAVLQSS 297
QY      61  GLYSLSVVTVPSSSLGTQTYICNNHKSNTKVDKVEPKSCDKTHTCPCPAPABELLG 120
DB      238  GLYSLSVVTVPSSSLGTQTYICNNHKSNTKVDKVEPKSCDKTHTCPCPAPABELLG 357
QY      121  PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAKTRPREEOYN 180
DB      358  PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAKTRPREEOYN 417
QY      181  STYRVSVLTVLHQMWNNGKEYCKVSNKALPAPIEKTIISKAKQPREPOVYTLPPSRDE 240
DB      418  STYRVSVLTVLHQMWNNGKEYCKVSNKALPAPIEKTIISKAKQPREPOVYTLPPSRDE 477
QY      241  LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
DB      478  LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 537
QY      301  QOGNVFSCSVMEALAHNHYQORSLSLSPGK 330
DB      538  QOGNVFSCSVMEALAHNHYQORSLSLSPGK 567

RESULT 11
US-09-746-359A-53
; Sequence 53, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenteng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jasper, Stephen R.
; APPLICANT: Chandrasekhar, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-746-359A-53

Query Match          98.0%; Score 1729; DB 4; Length 571;
Best Local Similarity 97.9%; Pred. No. 6.1e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1  ASTGPPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMNSGALTSGVHTFPAVLQSS 60
DB      242  ASTGPPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMNSGALTSGVHTFPAVLQSS 301
QY      61  GLYSLSVVTVPSSSLGTQTYICNNHKSNTKVDKVEPKSCDKTHTCPCPAPABELLG 120
DB      302  GLYSLSVVTVPSSSLGTQTYICNNHKSNTKVDKVEPKSCDKTHTCPCPAPABELLG 361
```



QY	121	PSVLPFPKPKDPTLMI	SSTPEVTCVVVDVSHEDPEVKFNWYVDGVEAHNKT	KPREEOYN	180
Db	362	PSVLPFPKPKDPTLMI	SSTPEVTCVVVDVSHEDPEVKFNWYVDGVEAHNKT	KPREEOYN	421
QY	181	STYRVSVLTVLHQNMMNGKE	YCKCKVSNKALPAPIEKTI	ISAKVQPREQVYTLPPSRDE	240
Db	422	STYRVSVLTVLHQNMMNGKE	YCKCKVSNKALPAPIEKTI	ISAKVQPREQVYTLPPSRDE	481
QY	241	LTKNQVSLTCLVKGF	YPSDIAVEMESNQPRENNYKTPRPVLDS	VCSFLLYSKLTVDKSRM	300
Db	482	LTKNQVSLTCLVKGF	YPSDIAVEMESNQPRENNYKTPRPVLDS	VCSFLLYSKLTVDKSRM	541
QY	301	QCGNVFSCSVNHEALHNHY	IQOQRLSLSLSPGK	330	
Db	542	QCGNVFSCSVNHEALHNHY	IQOQRLSLSLSPGK	571	
RESULT 12					
US-09-313-942-9					
; Sequence 9, Application US/09313942					
; Patent No. 6472179					
; GENERAL INFORMATION:					
; APPLICANT: REGENERON PHARMACEUTICALS, INC.					
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING					
; TITLE OF INVENTION: AND USING					
; FILE REFERENCE: REG 203-A					
; CURRENT APPLICATION NUMBER: US/09/313,942					
; PRIOR FILING DATE: 1999-05-19					
; PRIOR APPLICATION NUMBER: 09/313,942					
; PRIOR FILING DATE: 1999-05-19					
; PRIOR APPLICATION NUMBER: 60/101,858					
; PRIOR FILING DATE: 1998-09-25					
; NUMBER OF SEQ ID NOS: 32					
; SOFTWARE: FASTSEQ for Windows Version 3.0					
; SEQ ID NO 9					
; LENGTH: 951					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-09-313-942-9					
Query Match					
Best Local Similarity 96.0%; Score 1729; DB 4; Length 951;					
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0					
QY	1	ASTKGSPVFPLAPSSKSTSGGTAA	LGCLVKYQFPEPVTWYSNWVGAL	TSGVHFPFPAVLDS	60
Db	622	ASTGSPSVFPLAPSSKSTSGGTAA	LGCLVKDYFPEPVTWYSNWVGAL	TSGVHFPFPAVLDS	681
QY	61	GLYSLSVSVTVTPSSSLGTQTYI	CNVNHNKPSNTKVDKVEPKSCD	PTHCTPCPCAPABELLG	120
Db	682	GLYSLSVSVTVTPSSSLGTQTYI	CNVNHNKPSNTKVDKVEPKSCD	THCTPCPCAPABELLG	741
QY	121	PSVLPFPKPKDPTLMI	SSTPEVTCVVVDVSHEDPEVKFNWYVDGVEAHNKT	KPREEOYN	180
Db	742	PSVLPFPKPKDPTLMI	SSTPEVTCVVVDVSHEDPEVKFNWYVDGVEAHNKT	KPREEOYN	801
QY	181	STYRVSVLTVLHQNMMNGKE	YCKCKVSNKALPAPIEKTI	ISAKVQPREQVYTLPPSRDE	240
Db	802	STYRVSVLTVLHQNMMNGKE	YCKCKVSNKALPAPIEKTI	ISAKVQPREQVYTLPPSRDE	861
QY	241	LTKNQVSLTCLVKGF	YPSDIAVEMESNQPRENNYKTPRPVLDS	VCSFLLYSKLTVDKSRM	300
Db	862	LTKNQVSLTCLVKGF	YPSDIAVEMESNQPRENNYKTPRPVLDS	VCSFLLYSKLTVDKSRM	921
QY	301	QCGNVFSCSVNHEALHNHY	IQOQRLSLSLSPGK	330	
Db	922	QCGNVFSCSVNHEALHNHY	IQOQRLSLSLSPGK	951	
RESULT 13					
US-09-289-942A-7					
; Sequence 7, Application US/09289942A					

```

; Patent No. 6482928
; GENERAL INFORMATION:
; APPLICANT: Pat, Emil F.
; APPLICANT: Klein, Michel H.
; APPLICANT: Chong, Pele
; APPLICANT: Pedyczak, Arthur
; TITLE OF INVENTION: Fab-EPITOPE COMPLEX FROM THE HIV-1 CROSS-NEUTRALIZING
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 2F5
; FILE REFERENCE: 1038-926 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/289,942A
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 462
; TYPE: PR1
; ORGANISM: Human immunodeficiency virus type 1
; OS-09-289-942A-7

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Query Match	97.8%;	Score 1725;	DB 4;	Length 462;
Best Local Similarity	97.6%;	Pred. No. 1.1e-156;		
Matches .322;	Conservative	3;	Mismatches 5;	Indels 0;
			Gaps	0;

QY	1	ASTGPFVFPFLAPSPSKSTSGGTALGCVKYOFPPEPVTVMNNSGALTSGVHFFPVALDSS	60
Db	133	ASTGPFVFPFLAPSPSKSTSGGTALGCLVYDFFPEPVTVMNNSGALTSGVHFFPVALDSS	192
QY	61	GLYSLSSTVTPSSSLGTOTYICNVNHNKSPNTKDKVKEPKSCDKHTHCPCPABELLGG	120
Db	193	GLYSLSSTVTPSSSLGTOTYICNVNHNKSPNTKDKVKEPKSCDKHTHCPCPABELLGG	252
QY	121	PSVFLFPKPCKDTLMISRTPEBTCVVVDVSHEDPEVKNMVYDGYEVHNVKTPREEQYN	180
Db	253	PSVFLFPKPCKDTLMISRTPEBTCVVVDVSHEDPEVKNMVYDGYEVHNVKTPREEQYN	312
QY	181	STRVSVVLTVLHONMNMNGKEYKCKKVSNKALPAPLEKTSIAKQVOPREPOVYTLPPSRBE	240
Db	313	STRVSVVLTVLHODMNLNGKEYKCKKVSNKAPAPLEKTSIAKQGPRESPOVYTLPPSRBE	372
QY	241	LTKNQVSLTCLVKGFPSPDIAVEMESNQPENNNTKTPRPVLDVSFFLYSKLTVDKSRM	300
Db	373	LTKNQVSLTCLVKGFPSPDIAVEMESNQPENNNTKTPRPVLDSDGFFLYSKLTVDKSRM	432
QY	301	QQGNVFSQVMHEALHNHYOQRSLSLSPGK	330
Db	433	QQGNVFSQVMHEALHNHYTKSLSLSPGK	462

```

1      RESULT 14
2      US-09-740-002-27
3      ; Sequence 27, Application US/09740002
4      ; Patent No. 6537809
5      ; GENERAL INFORMATION:
6      ; APPLICANT: BRAMS, PETER
7      ; APPLICANT: MORROW, PHILLIP
8      ; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
9      ; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
10     ; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
11     ; FILE REFERENCE: 037003-0275759
12     ; CURRENT APPLICATION NUMBER: US/09/740,002
13     ; CURRENT FILING DATE: 2000-12-20
14     ; PRIOR APPLICATION NUMBER: 09/335,697
15     ; PRIOR FILING DATE: 1999-06-18
16     ; PRIOR APPLICATION NUMBER: 08/488,376
17     ; PRIOR FILING DATE: 1995-06-07
18     ; NUMBER OF SEQ ID NOS: 27
19     ; SOFTWARE: PatentIn Ver. 2.1
20     ; SEQ ID NO 27
21     ; LENGTH: 475
22     ; TYPE: PR1
23     ; ORGANISM: Homo sapiens
24     ; US-09-740-002-27

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Query Match 97.8%; Score 1725; DB 4; Length 475;  
Best Local Similarity 97.6%; Pred. No. 1.1e-156;  
Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVLQSS 60  
DB 146 ASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVLQSS 205  
QY 61 GLYSLSVTVTPSSSLGTQTYICNNHKSNTKVDKVEPKSCDKHTHCPCPAPPELLGG 120  
DB 206 GLYSLSVTVTPSSSLGTQTYICNNHKSNTKVDKVEPKSCDKHTHCPCPAPPELLGG 265  
QY 121 PSVFLEPPPKDXTLMSRTEVTCVVDVSHEDPEVKFNMYDGYEVNHNKTKPREEOYN 180  
DB 266 PSVFLEPPPKDXTLMSRTEVTCVVDVSHEDPEVKFNMYDGYEVNHNKTKPREEOYN 325  
QY 181 STYRVSVLTVLHQMNGKEYCKVSNKALPAPIEKTIISKAKVOPREPOVYTLPPSRDE 240  
DB 326 STYRVSVLTVLHQMNGKEYCKVSNKALPAPIEKTIISKAKVOPREPOVYTLPPSRDE 385  
QY 241 LTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300  
DB 386 LTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 445  
QY 301 QQGNVFSCSVMEALAHNHYYQKRSLSLSPGK 330  
DB 446 QQGNVFSCSVMEALAHNHYYQKRSLSLSPGK 475

RESULT 15  
US-08-487-550-4  
; Sequence 4, Application US/08487550  
; Patent No. 613898  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Releasee #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,550  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teekin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 476 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-487-550-4

Query Match 97.8%; Score 1725; DB 3; Length 476;  
Best Local Similarity 97.6%; Pred. No. 1.1e-156;

Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVLQSS 60  
DB 147 ASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVLQSS 206  
QY 61 GLYSLSVTVTPSSSLGTQTYICNNHKSNTKVDKVEPKSCDKHTHCPCPAPPELLGG 120  
DB 207 GLYSLSVTVTPSSSLGTQTYICNNHKSNTKVDKVEPKSCDKHTHCPCPAPPELLGG 266  
QY 121 PSVFLEPPPKDXTLMSRTEVTCVVDVSHEDPEVKFNMYDGYEVNHNKTKPREEOYN 180  
DB 267 PSVFLEPPPKDXTLMSRTEVTCVVDVSHEDPEVKFNMYDGYEVNHNKTKPREEOYN 326  
QY 181 STYRVSVLTVLHQMNGKEYCKVSNKALPAPIEKTIISKAKVOPREPOVYTLPPSRDE 240  
DB 327 STYRVSVLTVLHQMNGKEYCKVSNKALPAPIEKTIISKAKVOPREPOVYTLPPSRDE 386  
QY 241 LTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300  
DB 387 LTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 446  
QY 301 QQGNVFSCSVMEALAHNHYYQKRSLSLSPGK 330  
DB 447 QQGNVFSCSVMEALAHNHYYQKRSLSLSPGK 476

Search completed: June 7, 2005, 09:04:00  
Job time : 47.1658 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 08:48:08 ; Search time 24.4421 Seconds  
(without alignments)  
913.271 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260  
Sequence: 1 EPRKCDKTHTCPPCPAPEL.....MHEALHNYQORSLSLSPK 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	97.2	330	1 GHU	Ig gamma-1 chain C
2	1219	96.7	374	2 S69339	Ig heavy chain V r
3	1217	96.6	255	4 S31866	Ig gamma-1 chain C
4	1172	93.0	234	2 PT0207	Ig gamma chain C r
5	1138	90.3	377	2 A23511	Ig gamma-3 chain C
6	1136	90.2	377	2 A60764	Ig gamma-3 chain C
7	1123	89.1	289	1 G3HWT1	Ig gamma-3 heavy C
8	1107	87.9	326	1 G2HU	Ig gamma-2 chain C
9	1097	87.1	327	1 G4HU	Ig gamma-4 chain C
10	883	70.1	323	1 GHRB	Ig gamma chain C r
11	868.5	68.9	328	2 I47160	Ig gamma 2b chain
12	868.5	68.9	328	2 I47159	Ig gamma 2a chain
13	865	68.7	277	2 I47162	Ig gamma 4 chain C
14	858	68.1	329	1 G2GP	Ig gamma-2 chain C
15	847.5	67.3	328	2 I47158	Ig gamma 1 chain C
16	840.5	66.7	328	2 I47161	Ig gamma 3 chain C
17	820	65.1	470	2 S22080	Ig heavy chain pre
18	813	64.5	323	2 PS0018	Ig gamma-2b chain
19	812.5	64.5	329	1 G3MSC	Ig gamma-3 chain C
20	811.5	64.4	308	2 C30554	Ig heavy chain C r
21	811.5	64.4	472	2 S31459	Ig gamma-1 chain C
22	801.5	63.6	398	1 G3MSM	Ig gamma-1 chain C
23	794.5	63.1	444	2 PC4436	monoclonal antiod
24	789.5	62.7	324	1 G1MS	Ig gamma-1 chain C
25	784.5	62.3	326	2 PS0017	Ig gamma-1 chain C
26	784.5	62.3	393	1 G1MSM	Ig gamma-1 chain C
27	776.5	61.6	329	1 S00847	Ig gamma-2c chain
28	776	61.6	330	1 G2MSA	Ig gamma-2a chain
29	776	61.6	469	2 S37483	Ig gamma-2a chain

30	772	61.3	335	1 G2MSAB	Ig gamma-2a chain
31	771	61.2	399	1 G2MSAM	Ig gamma-2a chain
32	761	60.4	446	2 S40295	Ig gamma-2a chain
33	751.5	59.6	474	1 G2MS11	Ig gamma-2b chain
34	747.5	59.3	322	2 PS0019	Ig gamma-2a chain
35	746.5	59.2	405	1 G2MSBM	Ig gamma-2b chain
36	735	58.3	327	2 S06611	Ig gamma-2 chain C
37	731.5	58.1	475	2 S01321	Ig gamma-2b chain
38	669	53.1	180	2 I46732	Ig gamma heavy cha
39	549	43.6	249	2 S69340	Ig heavy chain VHI
40	547	43.4	218	2 A36040	Ig heavy chain V-I
41	542	43.0	152	2 S14236	Ig gamma-1 chain C
42	366.5	29.1	572	2 B46529	Ig gamma-1 chain C
43	357	28.3	549	2 S04845	Ig heavy chain pre
44	353	28.0	343	2 S25644	Ig mu chain C regi
45	353	28.0	455	1 MHMS	Ig mu chain C regi

## ALIGNMENTS

### RESULT 1

GHU  
Ig gamma-1 chain C region - human  
C/Species: Homo sapiens (man)  
C/Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004  
C/Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146  
R/Elison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982  
A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.  
A/Reference number: A93433; MUID:82274238; PMID:6287432  
A/Accession: A93433  
A/Molecule type: DNA  
A/Residues: 1-330 <EHL>  
A/Cross-references: UNIPROT:P01957; EMBL:Z17370  
A/Note: this sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) markers, 2 R/Harris, L.J.  
submitted to the EMBL Data Library, October 1992  
A/Reference number: S33904  
A/Accession: S36861  
A/Molecule type: DNA  
A/Residues: 2-330 <HAR>  
A/Cross-references: EMBL:Z17370  
R/Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.  
Cell 29, 671-679, 1982  
A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of a C  
A/Reference number: S33887; MUID:83001943; PMID:6811139  
A/Accession: S33887  
A/Molecule type: DNA  
A/Residues: 88-113;235-330 <TRK>  
A/Cross-references: EMBL:Z17370  
R/Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C  
Biochemistry 9, 3161-3170, 1970  
A/Title: The covalent structure of a human gammag2-immunoglobulin. VII. Amino acid sequenc  
A/Reference number: A90563; MUID:71064024; PMID:5489771  
A/Contents: myeloma protein Bu  
A/Accession: B90563  
A/Molecule type: protein  
A/Residues: 1-96,'R',98-135 <CUN>  
A/Note: this sequence has the Gln(3) marker, 97-Arg  
R/Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970  
A/Title: The covalent structure of a human gammag2-immunoglobulin. VIII. Amino acid sequen  
A/Reference number: A90564; MUID:71064025; PMID:5530842  
A/Contents: Bu  
A/Accession: A90564  
A/Molecule type: protein  
A/Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'B',240,'  
A/Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met  
Hofpe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A/Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

Igen Primerstruktur.  
A:Reference number: A91668; MUID:77070269; PMID:826475  
A:Contents: myeloma protein N1e  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27  
A>Note: this sequence has the G1m(17) and G1m(1) markers  
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A:Title: Die Primerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL  
A:Reference number: A91723; MUID:83289131; PMID:6884994  
A:Contents: myeloma protein KOL; disulfide bonds  
A:Accession: A91723  
A:Molecule type: protein  
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'W', 242-266, 'D', 268-271, 'D', 273-330 <SCH  
A>Note: this sequence has the G1m(3) and G1m(non-1) markers  
R:Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A:Reference number: A90565; MUID:771064027; PMID:4923144  
A:Contents: annotation; disulfide bonds  
R:Dirker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
endbromide cleavage products, and the disulfide bridges.  
A:Reference number: A91667; MUID:77070267; PMID:1002129  
A:Contents: annotation; disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG1  
A:Cross-references: GDB:120085; OMIM:147100  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1, 114/1, 224/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa  
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1d  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM2>  
F:137-206/Domain: immunoglobulin homology <IM3>  
F:243-310/Domain: immunoglobulin homology <IM3>  
F:127-83,144-204,250-308/Disulfide bonds: #status experimental  
F:103/Disulfide bonds: interchain (to light chain) #status experimental  
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 97.2%; Score 1225; DB 1; Length 330;  
Best Local Similarity 97.0%; Pred. No. 3.5e-85;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 99 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 158  
QY 61 NMYVDGVEVHANKTPREBQYNSTRVSVLTVLHQMNMNGKEYCKVSNKALPAPIEKT 120  
DB 159 NMYVDGVEVHANKTPREBQYNSTRVSVLTVLHQMNMNGKEYCKVSNKALPAPIEKT 218  
QY 121 ISKATVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 180  
DB 219 ISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 278  
QY 161 PVLDSVGSFFLYSKLTVDKSRWQGNVSCSYMHKALHNHYTQKSLSLSPGK 232  
DB 279 PVLDSVGSFFLYSKLTVDKSRWQGNVSCSYMHKALHNHYTQKSLSLSPGK 330

RESULT 2  
S69339  
Ig heavy chain V region precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C:Accession: S69339; S72664  
R:Khamilchi, A.A.; Auconturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995

A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; MUID:95262687; PMID:7744049  
A:Accession: S69339  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <KHA>  
A:Cross-references: EMBL:X81695  
R:Khamilchi, A.A.  
Submitted to the EMBL Data Library, September 1994  
A:Reference number: S72664  
A:Accession: S72664  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140, 'C', 142-374 <KH2>  
A:Cross-references: EMBL:X81695  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 96.7%; Score 1219; DB 2; Length 374;  
Best Local Similarity 96.1%; Pred. No. 1.2e-84;  
Matches 223; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 143 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 202  
QY 61 NMYVDGVEVHANKTPREBQYNSTRVSVLTVLHQMNMNGKEYCKVSNKALPAPIEKT 120  
DB 203 NMYVDGVEVHANKTPREBQYNSTRVSVLTVLHQMNMNGKEYCKVSNKALPAPIEKT 262  
QY 121 ISKATVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 180  
DB 263 ISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 322  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVSCSYMHKALHNHYTQKSLSLSPGK 232  
DB 323 PVLDSVGSFFLYSKLTVDKSRWQGNVSCSYMHKALHNHYTQKSLSLSPGK 374

RESULT 3  
S31866  
Ig gamma-1 chain C region - synthetic  
C:Species: synthetic  
A>Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C:Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C:Accession: S31866  
R:Filipula, D.  
Submitted to the EMBL Data Library, February 1993  
A:Description: Screening method for protein-protein interactions of cloned gene products.  
A:Reference number: S31866  
A:Accession: S31866  
A:Molecule type: mRNA  
A:Residues: 1-255 <FIL>  
A:Cross-references: EMBL:X70421; NID:g33068; PID:CAA49866.1; PID:g33069  
C:Keywords: immunoglobulin  
F:1-22/Region: Escherichia coli outer membrane protein A precursor  
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 96.6%; Score 1217; DB 4; Length 255;  
Best Local Similarity 96.6%; Pred. No. 1e-84;  
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 24 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 83  
QY 61 NMYVDGVEVHANKTPREBQYNSTRVSVLTVLHQMNMNGKEYCKVSNKALPAPIEKT 120  
DB 84 NMYVDGVEVHANKTPREBQYNSTRVSVLTVLHQMNMNGKEYCKVSNKALPAPIEKT 143  
QY 121 ISKATVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 180  
DB 144 ISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 203

OY 161 PVLDSGSEFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYOQRSLSPGK 232  
 |||||  
 DB 204 PVLDSGSEFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYOQRSLSPGK 255

## RESULT 4

PT0207  
 Ig gamma chain C region - chimpanzee  
 C/Species: Pan troglodytes (chimpanzee)  
 C/Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 16-Jul-1999  
 C/Accession: PT0207  
 R/Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.  
 Mol. Immunol. 28, 319-322, 1991  
 A>Title: Nucleotide sequence of chimpanzee Cc and hinge regions.  
 A/Reference number: PT0207; MUID:91287716; PMID:2062315  
 A/Accession: PT0207  
 A/Molecule type: mRNA  
 A/Residues: 1-234 <EHR>  
 C/Supertfamily: Immunoglobulin C region; immunoglobulin homology  
 C/Keywords: immunoglobulin  
 F/48-117/Domain: immunoglobulin homology <IMM>

Query Match 93.0%; Score 1172; DB 2; Length 234;  
 Best Local Similarity 95.6%; Pred. No. 2.3e-81;  
 Matches 215; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 EPKSCDKHTHTCPCPAPPELLGSPSVLPFPKPKDTLMTSRTEVTCVVVDVSHEDPEVKF 60  
 |||||  
 DB 10 EPKSCDTHTHTCPCPAPPELLGSPSVLPFPKPKDTLMTSRTEVTCVVVDVSHEDPEVKF 69  
 |||||  
 OY 61 NMYVDGVEVHNKTKPREEQNSTYRVSVLTFLHQNMMNGEKYCKVSNKALPAPIEKT 120  
 |||||  
 DB 70 NMYVDGVEVHNKTKPREEQNSTYRVSVLTFLHQMNLNGEKYCKVSNKALPAPIEKT 129  
 |||||  
 OY 121 ISKAVQPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGOPENNYKTP 180  
 |||||  
 DB 130 ISKAGQPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGOPENNYKTP 189  
 |||||  
 OY 181 PVLDSGSEFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYOQRSLSPGK 225  
 |||||  
 DB 190 PVLDSGSEFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYOQRSLSPGK 234  
 |||||

## RESULT 5

A23511  
 Ig gamma-3 chain C region (allotype G3m(b)) - human  
 C/Species: Homo sapiens (man)  
 C/Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
 C/Accession: A23511  
 R/Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
 Nucleic Acids Res. 14, 1779-1789, 1986  
 A>Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cDNA  
 A/Reference number: A23511; MUID:86148507; PMID:3081877  
 A/Accession: A23511  
 A/Molecule type: DNA  
 A/Residues: 1-377 <HUC>  
 A/Cross-references: GB:X03604; GB:M12958; NID:G33070; PIDN:CAA27268.1; PID:G577056

C/Species: Homo sapiens (man)  
 C/Date: 31-Dec-1979 #sequence\_revision 23-Oct-1981 #text\_change 16-Jul-1999  
 C/Accession: A90442; A92219; A93915; A02149  
 R/Frangione, B.; Rosenwasser, E.; Prell, F.; Franklin, E.C.  
 Biochemistry 19, 4304-4308, 1980  
 A>Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-chain  
 A/Reference number: A90442; MUID:81021548; PMID:6774747  
 A/Accession: A90442  
 A/Content: heavy chain disease protein W18  
 A/Accession: A90442  
 A/Molecule type: protein  
 A/Residues: 1-289 <FRA>  
 A/Note: this molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain  
 A/Note: the sequence of residues 42-76 was taken from the reference that follows  
 J. Biol. Chem. 252, 883-889, 1977

Query Match 90.3%; Score 1136; DB 2; Length 377;  
 Best Local Similarity 89.7%; Pred. No. 1.5e-78;  
 Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

OY 1 EPKSCDKHTHTCPCPAPPELLGSPSVLPFPKPKDTLMTSRTEVTCVVVDVSHEDPEVKF 60  
 |||||  
 DB 146 EPKSCDTHTHTCPCPAPPELLGSPSVLPFPKPKDTLMTSRTEVTCVVVDVSHEDPEVKF 205  
 |||||

OY 61 NMYVDGVEVHNKTKPREEQNSTYRVSVLTFLHQNMMNGEKYCKVSNKALPAPIEKT 120  
 |||||  
 DB 206 NMYVDGVEVHNKTKPREEQNSTYRVSVLTFLHQMNLNGEKYCKVSNKALPAPIEKT 265  
 |||||

OY 121 ISKAVQPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGOPENNYKTP 180  
 |||||  
 DB 266 ISKTRGQPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGOPENNYKTP 325  
 |||||

OY 181 PVLDSGSEFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYOQRSLSPGK 232  
 |||||  
 DB 326 PVLDSGSEFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYOQRSLSPGK 377  
 |||||

## RESULT 6

A60764  
 Ig gamma-3 chain C region, form LAT - human  
 C/Species: Homo sapiens (man)  
 C/Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004  
 C/Accession: A60764  
 R/Huck, S.; Lefranc, G.; Lefranc, M.P.  
 Immunogenetics 30, 250-257, 1989  
 A>Title: A human immunoglobulin IGHC3 allele (Gmb0, b1, c3, c5, v) with an IGHC4 convert  
 A/Reference number: A60764; MUID:90007613; PMID:2571587  
 A/Accession: A60764  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-377 <HUC>  
 A/Cross-references: UNIPROT:Q8N4Y9  
 C/Supertfamily: Immunoglobulin C region; immunoglobulin homology  
 C/Keywords: immunoglobulin  
 F/20-85/Domain: immunoglobulin homology <IMM>

Query Match 90.2%; Score 1136; DB 2; Length 377;  
 Best Local Similarity 89.7%; Pred. No. 2.1e-78;  
 Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

OY 1 EPKSCDKHTHTCPCPAPPELLGSPSVLPFPKPKDTLMTSRTEVTCVVVDVSHEDPEVKF 60  
 |||||  
 DB 146 EPKSCDTHTHTCPCPAPPELLGSPSVLPFPKPKDTLMTSRTEVTCVVVDVSHEDPEVKF 205  
 |||||  
 OY 61 NMYVDGVEVHNKTKPREEQNSTYRVSVLTFLHQNMMNGEKYCKVSNKALPAPIEKT 120  
 |||||  
 DB 206 NMYVDGVEVHNKTKPREEQNSTYRVSVLTFLHQMNLNGEKYCKVSNKALPAPIEKT 265  
 |||||  
 OY 121 ISKAVQPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGOPENNYKTP 180  
 |||||  
 DB 266 ISKTRGQPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGOPENNYKTP 325  
 |||||  
 OY 181 PVLDSGSEFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYOQRSLSPGK 232  
 |||||  
 DB 326 PVLDSGSEFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYOQRSLSPGK 377  
 |||||

## RESULT 7

G3H0W1  
 Ig gamma-3 heavy chain disease proteins - human  
 C/Species: Homo sapiens (man)  
 C/Date: 31-Dec-1979 #sequence\_revision 23-Oct-1981 #text\_change 16-Jul-1999  
 C/Accession: A90442; A92219; A93915; A02149  
 R/Frangione, B.; Rosenwasser, E.; Prell, F.; Franklin, E.C.  
 Biochemistry 19, 4304-4308, 1980  
 A>Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-chain  
 A/Reference number: A90442; MUID:81021548; PMID:6774747  
 A/Accession: A90442  
 A/Content: heavy chain disease protein W18  
 A/Accession: A90442  
 A/Molecule type: protein  
 A/Residues: 1-289 <FRA>  
 A/Note: this molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain  
 A/Note: the sequence of residues 42-76 was taken from the reference that follows  
 J. Biol. Chem. 252, 883-889, 1977

A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication  
A:Reference number: A92219, MUID:77118661, PMID:402363  
A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W  
A:Accession: A92219  
A:Molecule type: protein  
A:Residues: 12-97 <MIC>  
A>Note: the hinge region in gamma-3 chains is about four times as long as in other gamma  
idue segment (12-28)  
A>Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter  
R:Wolfsenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.  
Biochem. Biophys. Res. Commun. 71, 907-914, 1976  
A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the  
A:Reference number: A90198; MUID:77021516; PMID:823945  
A:Contents: heavy chain disease protein ZUC, partial sequence corresponding to residues  
A:Accession: A90198  
A:Molecule type: protein  
A:Residues: 59-125, 'E', 128-226, 228-289 <NOI>  
A>Note: this protein lacks most of the V region, all of the CH1 region, and part of the  
R:Alexander, A.; Steilmeier, M.; Barltan, D.; Frangione, B.; Franklin, E.C.; Hood, L.;  
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982  
A:Title: gamma heavy chain disease in man: CDNA sequence supports partial gene deletion  
A:Reference number: A93915, MUID:82247835, PMID:8608505  
A:Contents: heavy chain disease protein Omm  
A:Accession: A93915  
A:Molecule type: mRNA  
A:Residues: 12-70, 72-114, 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157  
A>Note: a carboxyl-terminal lys is removed posttranslationally  
A:Note: this sequence may represent an allelic form or another gamma chain sublaas  
A:Comment: The heavy chain disease protein Wis is shown.  
C:Genetics:  
A:Gene: GDB:IGHG3  
A:Cross-references: GDB:119339, OMIM:147120  
A:Map position: 14q32.33-14q32.33  
C:Superfamily: Immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglyutamic acid  
F:203-270/Domain: immunoglobulin homology <IMI>  
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
F:6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental  
Query Match 89.1%; Score 1123; DB 1; Length 289;  
Best Local Similarity 88.3%; Pred. No. 1.5e-77;  
Matches 204; Conservative 14; Mismatches 13; Indels 0; Gaps 0;  
Qy 1 EPKSCDKHTHTCPCPAPRLGSPSVFLPPPKKDTLMSRTPEVYCVVVDVSHEDPEYKF 60  
Db 59 EPKSCDTPPCPCPCAPRLGSPSVFLPPPKKDTLMSRTPEVYCVVVDVSHEDPEYQF 118  
Qy 61 NWYDGVENVHVKTKPREEQYNSTYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
Db 119 KMYDGVQVHNAKTKPREEQYFSTYRVSVLTVLHQNMDGKEYCKVSNKALPAPIEKT 178  
Qy 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
Db 179 ISKTKGQPREPOVYTLPPSRDEMTKNQVSLTCLVKGFPYSDIAVWESNGQENNYKTTP 238  
Qy 181 PVLDSVGSFELYSKLTVDKSRWQQGNVSCSYMEALHNHVOORSLSLSPG 231  
Db 239 PVLDSVGSFELYSKLTVDKSRWQQGNVSCSYMEALHNHVOORSLSLSPG 289  
RESULT 8  
G2HU  
19 gamma-2 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #ext\_change 09-Jul-2004  
C:Accession: A93906; A92809; A90752; A93132; A02148  
R:Ellison, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
A:Reference number: A93906, MUID:82197621, PMID:6804948  
A:Accession: A93906  
A:Molecule type: DNA  
A:Residues: 1-326 <ELL>

A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:932759; PIDN:CA858438.1; P1  
A>Note: Lys-326 is probably removed posttranslationally  
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and fi  
A:Reference number: A92809; MUID:81007873; PMID:6774012  
A:Contents: myeloma protein T11  
A:Accession: A92809  
A:Molecule type: protein  
A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>  
A>Note: Trp-156 is at or near the complement-binding site  
R:Comell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A:Title: The amino acid sequences of the three heavy chain constant region domains of a  
A:Reference number: A90752; MUID:80001357; PMID:113060  
A:Contents: myeloma protein Zie  
A:Accession: A90752  
A:Molecule type: protein  
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-;  
A>Note: this sequence has since been revised  
R:Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin G  
A:Reference number: A93132; MUID:80114419; PMID:118920  
A:Contents: Zie  
A:Accession: A93132  
A:Molecule type: protein  
A:Residues: 238-275 <HOF>  
R:Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A:Reference number: A94591  
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A>Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic  
ned  
R:Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A:Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.  
A:Reference number: A90253; MUID:72033500; PMID:4949472  
A:Contents: annotation; myeloma protein Sa, disulfide bonds  
R:Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A:Title: Structural studies of immunoglobulin G.  
A:Reference number: A93157; MUID:69064124; PMID:5782707  
A:Contents: annotation; Sa, disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG2  
A:Cross-references: GDB:119338, OMIM:147110  
A:Map position: 14q32.33-14q32.33  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lat  
C:Superfamily: Immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IMI>  
F:133-202/Domain: immunoglobulin homology <IM2>  
F:239-306/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,140-200,246-304/Disulfide bonds: #status experimental  
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 87.9%; Score 1107; DB 1; Length 326;  
Best Local Similarity 88.4%; Pred. No. 2.8e-76;  
Matches 205; Conservative 12; Mismatches 11; Indels 4; Gaps 2;  
Qy 1 EPKSCDKHTHTCPCPAPRLGSPSVFLPPPKKDTLMSRTPEVYCVVVDVSHEDPEYKF 60  
Db 99 ERKCVF---CPKCAPP-VAGSPSVFLPPPKKDTLMSRTPEVYCVVVDVSHEDPEYQF 154  
Qy 61 NWYDGVENVHVKTKPREEQYNSTYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
Db 155 NWYDGVENVHNAKTKPREEQYFSTYRVSVLTVLHQNMDGKEYCKVSNKALPAPIEKT 214  
Qy 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180

Db 215 ISKTKGQREPOVYTLPPSRREMTNQVSLTCLVGFYPSDLAVEMESNGOPENNYKTTTP 274  
 Oy 181 PVLDSVGSFFLYSKLTVKSRMQGNVSCSVMEHAIHHNYOQRSLISLSPGK 232  
 Db 275 PMLSDSGFFLYSKLTVKSRMQGNVSCSVMEHAIHHNYOQRSLISLSPGK 326

## RESULT 9

G4HU

Ig gamma-4 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004

C/Accession: A90933; A90249; A02150

R/Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A/Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A/Reference number: A90933; MUID:83157104; PMID:6293662

A/Accession: A90933

A/Molecule type: DNA

A/Residues: 1-327 &lt;ELL&gt;

A/Cross-references: UNIPROT:P01861

A/Note: the sequence was determined from the germ-line gene

R/Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A/Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant

A/Reference number: A90249; MUID:70207560; PMID:4192699

A/Accession: A90249

A/Molecule type: protein

A/Residues: 1-30; 81-326 &lt;PIN&gt;

C/Genetics:

A/Gene: GDB:IGHG4

A/Cross-references: GDB:119340; OMIM:147130

A/Map position: 14q32.33-14q32.33

A/Intons: 99/1; 111/1; 221/1

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into 1a

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology &lt;IM1&gt;

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology &lt;IM2&gt;

F:240-307/Domain: immunoglobulin homology &lt;IM3&gt;

F:14/Distal disulfide bonds: interchain (to light chain) #status experimental

F:127-83; 141-201; 247-305/Distal disulfide bonds: #status predicted

F:106; 109/Distal disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 87.1%; Score 1097; DB 1; Length 327;

Best Local Similarity 90.5%; Pred. No. 1.6e-75;

Matches 201; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Oy 11 CPKPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNYYVDGVEVH 70  
 Db 106 CPKPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNYYVDGVEVH 165  
 Oy 71 NKTTPREQVNSTRVVSVLT/LVHOMNMGKEYCKVSNKALPAPIETKISKAKQPRE 130  
 Db 166 NAKTPREQVNSTRVVSVLT/LVHOMNMGKEYCKVSNKALPAPIETKISKAKQPRE 225  
 Oy 131 PoyVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTTPVLDVSGSF 190  
 Db 226 PoyVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTTPVLDVSGSF 285  
 Oy 191 LYSKLTVDKSRMVGFSVMEHAIHHNYOQRSLISLSPGK 232  
 Db 286 LYSKLTVDKSRMVGFSVMEHAIHHNYOQRSLISLSPGK 327

## RESULT 10

GHRB

Ig gamma chain C region - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 24-Apr-1984 #sequence\_revision 15-Nov-1984 #text\_change 09-Jul-2004  
 C/Accession: A91749; A90290; A93928; A90245; A94416; A02161  
 R/Bernstein, K.E.; Alexander, C.B.; Mage, R.G.  
 Immunogenetics 18, 387-397, 1983  
 A/Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-1 haploty

A/Reference number: A91749; MUID:84030930; PMID:6313520

A/Accession: A91749

A/Molecule type: mRNA

A/Residues: 1-323 &lt;BER&gt;

A/Cross-references: UNIPROT:P01870

A/Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr

R/Piracy, D.W.; Mole, L.E.

Biochem. J. 151, 337-349, 1975

A/Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob

A/Reference number: A90290; MUID:76135469; PMID:1243651

A/Accession: A90290

A/Molecule type: protein

A/Residues: 1-47; 'E', '49-71', 'PV', '72-128' &lt;PRA&gt;

R/Martens, C.L.; Moore, K.W.; Steimetz, M.; Hood, L.; Knight, K.L.

Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982

A/Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain

A/Reference number: A93928; MUID:83299917; PMID:6193512

A/Accession: A93928

A/Molecule type: mRNA

A/Residues: 88-103; 'W', '105-143', 'E', '145-184', 'A', '186', 'E', '188-266' &lt;MAR&gt;

A/Cross-references: GB:M6426; NID:9165111; PIDN:AA31289.1; PID:9165112

A/Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker

R/Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.

Biochem. J. 116, 249-259, 1970

A/Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin (

A/Reference number: A90245; MUID:70110015; PMID:5461106

A/Accession: A90245

A/Molecule type: protein

A/Residues: 132-143; 'E', '145-161' &lt;FRU&gt;

R/Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.

In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,

A/Reference number: A94416

A/Accession: A94416

A/Molecule type: protein

A/Residues: 129-131; 155-172, 'D', '174-184', 'A', '186', 'E', '188-200', 'D', '202-217', 'E', '219-232', 'Q', ';

A/Note: this has the e15 allotypic marker, 185-Ala

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into 1a

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-82/Domain: immunoglobulin homology &lt;IM1&gt;

F:130-199/Domain: immunoglobulin homology &lt;IM2&gt;

F:236-303/Domain: immunoglobulin homology &lt;IM3&gt;

F:173/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 70.1%; Score 893; DB 1; Length 323;

Best Local Similarity 64.5%; Pred. No. 2.2e-59;

Matches 160; Conservative 34; Mismatches 38; Indels 16; Gaps 2;

Oy 1 EPKSCDKTH-----TC-PPCPAPBELLGGPSVFLPPKPKDTLMISRTPEV 44  
 Db 76 CPVTGNVAHPAINTKVDKTVARSTCKPTCPPELLGGPSVFLPPKPKDTLMISRTPEV 135  
 Oy 45 TCVVVDVSHEDPEVKFNYYVDGVEVHNYKTRREQVNSTRVVSVLT/LVHOMNMGKEY 104  
 Db 136 TCVVVDVSHEDPEVKFNYYVDGVEVHNYKTRREQVNSTRVVSVLT/LVHOMNMGKEY 195  
 Oy 105 KCKVSNKALPAPIETKISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 164  
 Db 196 KCKVSNKALPAPIETKISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 255  
 Oy 165 EWESNGOPENNYKTTTPVLDVSGSFVLYSKLTVKSRMQGNVSCSVMEHAIHHNYOQR 224  
 Db 256 EWEKNGKADENNYKTTTPVLDVSGSFVLYSKLTVKSRMQGNVSCSVMEHAIHHNYOQR 315  
 Oy 225 SISLSPGK 232  
 Db 316 SISLSPGK 323



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RESULT 11
147160
Ig gamma 2b chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: 147160
R/Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A/Reference number: 147158; MUID:95015845; PMID:7930579
A/Accession: 147160
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-328 <KAC>
A/Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C/Genetics:
C/Gene: IgG2b
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <Imm>

Query Match      68.9%; Score 868.5; DB 2; Length 328;
Best Local Similarity 70.1%; Pred. No. 2.8e-58;
Matches 157; Conservative 32; Mismatches 32; Indels 3; Gaps 2;

Db
11 CPGCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 70
106 CPICPACE-SPGPSVFIFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 164
71 NVKTRPREQVNSTRVVSVLTVLHQNMNKGKEYCKVSNKALPAPIETKISKAKVQPRE 130
165 TAQTRPKREQNSTRVVSVLPIQHODWLNGKEFKCKVNNKDLPAPIRITISKAKGQTR 224
131 PQVYTLPPSRDELTKQVSLTCLVKGFPYSDIAVESNGQ--PENNYKTPPVLDVSGS 188
225 PQVYTLPPHAELSRKSVITCLVIGFYPPDIDVEMQRNGQPEPEGNYRTTPPQDDVGT 284
189 FFLYSKLTVDKSRMOQGVNFGSCVMEHALHNHYOQRSLSLSPGK 232
285 YFLYSKFSVDKASWQGGIFQCAVMEHALHNHYTKSISKTPGK 328

RESULT 12
147159
Ig gamma 2a chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: 147159
R/Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A/Reference number: 147158; MUID:95015845; PMID:7930579
A/Accession: 147159
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-328 <KAC>
A/Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C/Genetics:
C/Gene: IgG2a
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <Imm>

Query Match      68.9%; Score 868.5; DB 2; Length 328;
Best Local Similarity 70.1%; Pred. No. 2.8e-58;
Matches 157; Conservative 32; Mismatches 32; Indels 3; Gaps 2;

Db
11 CPGCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 70
106 CPICPACE-SPGPSVFIFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 164
71 NVKTRPREQVNSTRVVSVLTVLHQNMNKGKEYCKVSNKALPAPIETKISKAKVQPRE 130
165 TAQTRPKREQNSTRVVSVLPIQHODWLNGKEFKCKVNNKDLPAPIRITISKAKGQTR 224
131 PQVYTLPPSRDELTKQVSLTCLVKGFPYSDIAVESNGQ--PENNYKTPPVLDVSGS 188
225 PQVYTLPPHAELSRKSVITCLVIGFYPPDIDVEMQRNGQPEPEGNYRTTPPQDDVGT 284
189 FFLYSKLTVDKSRMOQGVNFGSCVMEHALHNHYOQRSLSLSPGK 232
285 YFLYSKFSVDKASWQGGIFQCAVMEHALHNHYTKSISKTPGK 328
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Db
165 TAQTRPKREQNSTRVVSVLPIQHODWLNGKEFKCKVNNKDLPAPIRITISKAKGQTR 224
Qy
131 PQVYTLPPSRDELTKQVSLTCLVKGFPYSDIAVESNGQ--PENNYKTPPVLDVSGS 188
Db
225 PQVYTLPPHAELSRKSVITCLVIGFYPPDIDVEMQRNGQPEPEGNYRTTPPQDDVGT 284
Qy
189 FFLYSKLTVDKSRMOQGVNFGSCVMEHALHNHYOQRSLSLSPGK 232
285 YFLYSKFSVDKASWQGGIFQCAVMEHALHNHYTKSISKTPGK 328

RESULT 13
147162
Ig gamma 4 chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: 147162
R/Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A/Reference number: 147158; MUID:95015845; PMID:7930579
A/Accession: 147162
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-277 <KAC>
A/Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C/Genetics:
C/Gene: IgG4
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <Imm>

Query Match      68.7%; Score 865; DB 2; Length 277;
Best Local Similarity 69.0%; Pred. No. 4.1e-58;
Matches 158; Conservative 32; Mismatches 35; Indels 4; Gaps 3;

Db
8 THTCPPE-APPELLG-GPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 65
49 TTKTRPCPCICACEGPGSARIFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 108
66 GVEVHNKTRPREQVNSTRVVSVLTVLHQNMNKGKEYCKVSNKALPAPIETKISKAK 125
109 GVEVHTAQTRPKREQNSTRVVSVLPIQHODWLNGKEFKCKVNNKDLPAPIRITISKAK 168
126 VQPREPQVYTLPPSRDELTKQVSLTCLVKGFPYSDIAVESNGQ--PENNYKTPPVLD 183
169 GQTRPPQVYTLPPSRDELTKQVSLTCLVKGFPYSDIAVESNGQ--PENNYKTPPVLD 228
184 DSVGSFFLYSKLTVDKSRMOQGVNFGSCVMEHALHNHYOQRSLSLSPGK 232
229 DVDGTYFLYSKLTVDKSRMOQGVNFGSCVMEHALHNHYTKSISKTPGK 277

RESULT 14
GZGP
Ig gamma-2 chain C region - guinea pig
C/Species: Cavia porcellus (guinea pig)
C/Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
C/Accession: A94553; A90352; A90359; A90384; A90385; A02151
R/Tietemann, T.M.
submitted to the Aclae, April 1975
A/Reference number: A94553
A/Accession: A94553
A/Molecule type: Protein
A/Residues: 1-3 <TRI>
A/Cross-references: UNIPROT:P01862
R/Birchlein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A/Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am
A/Accession: A90352; MUID:71058471; PMID:533606
A/Molecule type: Protein
A/Residues: 4-68 <BIR>
R/Turner, K.J.; Cebra, J.J.
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**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 08:39:41 ; Search time 114.197 Seconds

(without alignment)  
1040.329 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260

Sequence: 1 EPKSCDKHTPCPCPAPPL.....MHEALHNHYQQRSLSPGK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_prot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1225	97.2	330	1 GCI_HUMAN	P01857 homo sapien
2	1225	97.2	465	2 Q6GMC6	Q6GMC6 homo sapien
3	1225	97.2	466	2 Q6IN78	Q6IN78 homo sapien
4	1225	97.2	469	2 Q7Z7P5	Q7Z7P5 homo sapien
5	1225	97.2	470	2 Q6B2A4	Q6B2A4 homo sapien
6	1225	97.2	472	2 Q7Z5W1	Q7Z5W1 homo sapien
7	1225	97.2	472	2 Q6N089	Q6N089 homo sapien
8	1225	97.2	475	2 Q6GMC7	Q6GMC7 homo sapien
9	1225	97.2	476	2 Q6GMC1	Q6GMC1 homo sapien
10	1225	97.2	479	2 Q6P08	Q6P08 homo sapien
11	1221	96.9	473	2 Q6P055	Q6P055 homo sapien
12	1221	96.9	475	2 Q6M2Q6	Q6M2Q6 homo sapien
13	1221	96.9	480	2 Q6N094	Q6N094 homo sapien
14	1221	96.9	481	2 Q6N097	Q6N097 homo sapien
15	1221	96.9	482	2 Q7Z351	Q7Z351 homo sapien
16	1219	96.7	348	2 Q6P2X1	Q6P2X1 homo sapien
17	1219	96.7	473	2 Q6M2V7	Q6M2V7 homo sapien
18	1219	96.7	478	2 Q6P181	Q6P181 homo sapien
19	1219	96.7	480	2 Q6P3F1	Q6P3F1 homo sapien
20	1218	96.7	475	2 Q6N096	Q6N096 homo sapien
21	1214	96.3	475	2 Q6N095	Q6N095 homo sapien
22	1214	96.3	544	2 Q6P095	Q6P095 homo sapien
23	1196	94.9	487	2 Q6S2L2	Q6S2L2 mus sp. tv
24	1138	90.3	354	2 Q86T12	Q86T12 homo sapien
25	1138	90.3	518	2 Q6N030	Q6N030 homo sapien
26	1134	90.0	521	2 Q8N4Y9	Q8N4Y9 homo sapien
27	1128	89.5	290	1 GC3_HUMAN	P01860 homo sapien
28	1123	89.1	509	2 Q8N1F7	Q8N1F7 homo sapien
29	1107	87.9	326	1 GC2_HUMAN	P01859 homo sapien
30	1107	87.9	417	2 Q6N093	Q6N093 homo sapien
31	1104	87.6	464	2 Q6M2U6	Q6M2U6 homo sapien

32	1102	87.5	465	2 Q6P6C4	Q6P6C4 homo sapien
33	1097	87.1	327	1 GC4_HUMAN	P01861 homo sapien
34	1097	87.1	473	2 Q8TC63	Q8TC63 homo sapien
35	1093	86.7	493	2 Q68CN4	Q68CN4 homo sapien
36	1088	86.3	476	2 Q6MZX7	Q6MZX7 homo sapien
37	983	70.1	323	1 GC_RABIT	P01870 oryctolagus
38	877.5	69.6	337	2 Q95M34	Q95M34 equus caball
39	858	68.1	329	1 GC2_CAVPO	P01862 cavia porce
40	813	64.5	333	1 GC8_RAT	P20761 rattus norv
41	812.5	64.5	329	1 GC3_MOUSE	P22436 mus musculu
42	812.5	64.5	470	2 Q7TMK1	Q7TMK1 mus musculu
43	801.5	63.6	303	2 Q6KAM2	Q6KAM2 mus musculu
44	801.5	63.6	398	1 GC3M_MOUSE	P03987 mus musculu
45	795.5	63.1	463	2 Q99LC4	Q99LC4 mus musculu

#### ALIGNMENTS

RESULT 1.

ID	GCI_HUMAN	STANDARD	PRT	330 AA.
AC	P01857			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	IG gamma-1 chain C region.			
OS	Name=IGHG1			
GN	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NC	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Billson J.W., Berson B.O., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RT	Waxdal M.J., Edelman G.M.;			
RL	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";			
RN	Biochemistry 9:3161-3170(1970).			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RT	Edelman G.M.;			
RL	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";			
RN	Biochemistry 9:3171-3181(1970).			
RP	[4]			
RX	SEQUENCE (MYELOMA PROTEIN NIE).			
RA	MEDLINE=77070269; PubMed=826475;			
RT	Ponertingl H., Hilschmann N.;			
RL	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";			
RN	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RP	[5]			
RX	SEQUENCE (MYELOMA PROTEIN KOL) AND DISULFIDE BONDS.			
RA	MEDLINE=83289131; PubMed=6884994;			
RT	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RL	"Three-dimensional structure determination of antipodites. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";			
RN	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RP	[6]			
RX	DISULFIDE BONDS.			
RA	MEDLINE=71064027; PubMed=4923144;			

RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.  
 RL Intrachain disulfide bonds.";  
 RL Biochemistry 9:3188-3196(1970).  
 RN [7]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=77070267; PubMed=1002129;  
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nle), I: purification and  
 RT characterization of the protein, the L- and H-chains, the cyanogen  
 RT bromide cleavage products, and the disulfide bridges.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=81208100; PubMed=7236608;  
 RA Deisenhofer J.;  
 RT "Crystallographic refinement and atomic models of a human Fc fragment  
 RT and its complex with fragment B of protein A from Staphylococcus  
 RT aureus at 2.9- and 2.8-A resolution.";  
 RL Biochemistry 20:2361-2370(1981).  
 CC -1- MISCELLANEOUS: Nle has the GIM(17) allotypic marker, 97-K, and the  
 CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the  
 CC -1- MISCELLANEOUS: Nle also differs in the amidation states of 35,  
 CC 116, 198, 269 and 272.  
 CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues  
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
 CC 268-272.  
 CC -1- MISCELLANEOUS: KOL also differs in the amidation states of  
 CC residues 198, 267 and 272.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 CC EMBL; J00228; AAC82527.1; ALT\_INIT.  
 DR PIR; A93433; GHNU.  
 DR PDB; 1A77; X-ray; H=1-103.  
 DR PDB; 1D5B; X-ray; B/H=1-101.  
 DR PDB; 1D5I; X-ray; H=1-101.  
 DR PDB; 1D6V; X-ray; H=1-101.  
 DR PDB; 1DN2; X-ray; A/B=120-326.  
 DR PDB; 1B4K; X-ray; A/B=106-329.  
 DR PDB; 1FC1; X-ray; A/B=106-329.  
 DR PDB; 1FC2; X-ray; D=106-329.  
 DR PDB; 1FCJ; X-ray; A=121-326.  
 DR PDB; 1H2H; X-ray; H/K=1-330.  
 DR PDB; 1I7Z; X-ray; B/D=1-103.  
 DR PDB; 1IIS; X-ray; A/B=107-330.  
 DR PDB; 1IIX; X-ray; A/B=107-330.  
 DR PDB; 1L6X; X-ray; A=120-326.  
 DR PDB; 1QOX; X-ray; A/B=119-330.  
 DR PDB; 2RCS; X-ray; H=1-103.  
 DR GeneW; HGNC:5525; IGHG1.  
 DR MIM; 147100; -  
 DR GO; GO:0005624; C:membrane fraction; NAS.  
 DR GO; GO:0003823; F:antigen binding; TAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; Ig; 3  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW 3D-structure; Direct protein sequencing; Glycoprotein;  
 KW Immunoglobulin C region; Immunoglobulin domain.  
 FT NON TER 1 98 CH1.  
 FT DOMAIN 1 98 Hinge.  
 FT DOMAIN 99 110

FT	DOMAIN	111	223	
FT	DOMAIN	224	330	
FT	DISULFID	27	83	
FT	DISULFID	103	103	
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FT	DISULFID	112	112	
FT	DISULFID	144	204	
FT	DISULFID	250	308	
FT	CARBOHYD	180	180	
FT	VARIANT	97	97	
FT	VARIANT	239	239	
FT	VARIANT	241	241	
FT	STRAND	23	24	
FT	STRAND	26	33	
FT	STRAND	38	38	
FT	STRAND	41	41	
FT	TURN	42	45	
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FT	HELIX	73	75	
FT	TURN	76	78	
FT	STRAND	82	87	
FT	TURN	88	91	
FT	STRAND	92	97	
FT	TURN	102	103	
FT	STRAND	122	126	
FT	HELIX	130	134	
FT	TURN	136	137	
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FT	STRAND	183	190	
FT	HELIX	193	197	
FT	TURN	198	199	
FT	STRAND	202	207	
FT	TURN	209	210	
FT	STRAND	215	219	
FT	STRAND	227	227	
FT	STRAND	230	234	
FT	HELIX	238	242	
FT	STRAND	245	256	
FT	STRAND	261	266	
FT	TURN	267	268	
FT	STRAND	269	270	
FT	STRAND	274	276	
FT	STRAND	280	281	
FT	TURN	283	284	
FT	STRAND	287	296	
FT	HELIX	297	301	
FT	TURN	302	303	
FT	STRAND	306	311	
FT	TURN	313	314	
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FT	STRAND	319	324	
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Query Match 97.2%; Score 1225; DB 1; Length 330;  
 Best Local Similarity 97.0%; Pred. No. 1.8e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 BPKSCDKHTCTPCPCAPRLGGPSVFLPPPKKDTLMTSRTPVYTCVYVDSHEDPEVKF 60  
 DB 99 BPKSCDKHTCTPCPCAPRLGGPSVFLPPPKKDTLMTSRTPVYTCVYVDSHEDPEVKF 158

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QY 61 NMYVDGEVHNVKTKPREQYNSTYRVSVLTFLVHONMNGKEYCKVSNKALPAPIEKT 120
DB 159 NMYVDGEVHNVKTKPREQYNSTYRVSVLTFLVHONMNGKEYCKVSNKALPAPIEKT 218
QY 121 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESGOPENNYKTP 180
DB 219 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESGOPENNYKTP 278
QY 181 PVLDSVGSFFLTKLTVDSKRMQGVNFGCSVMHEALHNHYOQRSLSISPGK 232
DB 279 PVLDSVGSFFLTKLTVDSKRMQGVNFGCSVMHEALHNHYOQRSLSISPGK 330

RESULT 2
O6GMX6 PRELIMINARY; PRT; 465 AA.
AC O6GMX6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-cells;
RX MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ushed T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullanly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DB EMBL; BC073766; AAH73766.1; -
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003587; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF07654; Cl-set: 3.
DR Pfam: PF00047; IG: 4.
DR SMART; SM00409; IG: 2.
DR SMART; SM00407; IG: 1.
DR SMART; SM00406; IG: 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS50835; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
Query Match 97.2%; Score 1225; DB 2; Length 465;
Best Local Similarity 97.0%; Pred. No. 2.8e-88;

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Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EFKSCDKHTTCCPCAPPELLGSPVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 234 EFKSCDKHTTCCPCAPPELLGSPVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 293
QY 61 NMYVDGEVHNVKTKPREQYNSTYRVSVLTFLVHONMNGKEYCKVSNKALPAPIEKT 120
DB 294 NMYVDGEVHNVKTKPREQYNSTYRVSVLTFLVHONMNGKEYCKVSNKALPAPIEKT 353
QY 121 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESGOPENNYKTP 180
DB 354 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESGOPENNYKTP 413
QY 181 PVLDSVGSFFLTKLTVDSKRMQGVNFGCSVMHEALHNHYOQRSLSISPGK 232
DB 414 PVLDSVGSFFLTKLTVDSKRMQGVNFGCSVMHEALHNHYOQRSLSISPGK 465

RESULT 3
O6IN78 PRELIMINARY; PRT; 466 AA.
AC O6IN78;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ushed T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullanly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DB EMBL; BC072419; AAH72419.1; -
DR HSP: P01861; IADO.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003587; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF07654; Cl-set: 3.
DR SMART; SM00409; IG: 2.
DR SMART; SM00407; IG: 1.
DR SMART; SM00406; IG: 1.
DR PROSITE; PS50835; IG_LIKE; 4.

```

DR PROSITE: PS00290; IG\_MHC; UNKNOWN 2.  
 SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCEDB81076E CRC64;  
 Query Match 97.2%; Score 1225; DB 2; Length 466;  
 Best Local Similarity 97.0%; Pred. No. 2.8e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 |||||  
 DB 235 EPKSCDKTHTCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 294  
 |||||  
 QY 61 NMVYDGVENHNAKTPREEOYNSTRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
 |||||  
 DB 295 NMVYDGVENHNAKTPREEOYNSTRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 354  
 |||||  
 QY 121 ISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180  
 |||||  
 DB 355 ISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 414  
 |||||  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232  
 |||||  
 DB 415 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 466  
 |||||

RESULT 4  
 0727P5 PRELIMINARY; PRT; 469 AA.  
 AC 0727P5;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE IGHG1 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 Bobak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Krzywinski M.I., Skalska U., Small D.E., Scherch A., Schein J.E.,  
 Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (APR-2003) to the EMBL/Genbank/DBJ databases.  
 DR EMBL, BC051328; AAH51328.1; -  
 DR HSSP, P01857; IHHZ.  
 DR InterPro, IPR007110; IG-like.  
 DR InterPro, IPR003597; IG\_c1.  
 DR InterPro, IPR003006; IG\_MHC.  
 DR InterPro, IPR003596; IG\_v.  
 DR Pfam, PF07654; C1-set; 3.  
 DR SMART, SMO0406; IGV; 1.

DR PROSITE: PS00835; IG LIKE; 4.  
 SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;  
 Query Match 97.2%; Score 1225; DB 2; Length 469;  
 Best Local Similarity 97.0%; Pred. No. 2.8e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 |||||  
 DB 238 EPKSCDKTHTCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 297  
 |||||  
 QY 61 NMVYDGVENHNAKTPREEOYNSTRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
 |||||  
 DB 298 NMVYDGVENHNAKTPREEOYNSTRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 357  
 |||||  
 QY 121 ISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180  
 |||||  
 DB 358 ISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 417  
 |||||  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232  
 |||||  
 DB 418 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 469  
 |||||

RESULT 5  
 06PJ4 PRELIMINARY; PRT; 470 AA.  
 AC 06PJ4;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 Bobak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 Krzywinski M.I., Skalska U., Small D.E., Scherch A., Schein J.E.,  
 Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL, BC018747; AAH18747.1; -  
 DR HSSP, P01861; IADQ.  
 DR InterPro, IPR003599; IG.  
 DR InterPro, IPR007110; IG-like.  
 DR InterPro, IPR003597; IG\_c1.  
 DR InterPro, IPR003006; IG\_MHC.  
 DR InterPro, IPR003596; IG\_v.



DR Pfam: PF07654; Cl-set: 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 470 AA; 51715 MW; 7849556A11FD7D9 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 470;  
Best Local Similarity 97.0%; Pred. No. 2.8e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPELLGGPSVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 239 EPKSCDKHTHTCPCPAPELLGGPSVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 298  
QY 61 NMVYDGEVHNKTKPREEQYNSTRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
DB 239 NMVYDGEVHNKTKPREEQYNSTRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 358  
QY 121 ISKAVQPREPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGOPENNYKTP 180  
DB 359 ISKAVQPREPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGOPENNYKTP 418  
QY 181 PVLDSGSEFFLYSKLTVDKSRWQGNVFCSVMEALHNHYOQRLSLSPGK 232  
DB 419 PVLDSGSEFFLYSKLTVDKSRWQGNVFCSVMEALHNHYOQRLSLSPGK 470

## RESULT 6

Q725W1 PRELIMINARY; PRT; 470 AA.

ID Q725W1  
AC Q725W1;  
DT 01-OCT-2003 (TRENBLrel. 25, Created)  
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Splice;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Gittwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Splice;  
RA Strusberg R.;  
RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BC053984; AAHS3984.1; -.  
DR HSP; F01857; IHZH.

DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG v.  
DR Pfam; PF07654; Cl-set: 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 470;  
Best Local Similarity 97.0%; Pred. No. 2.8e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPELLGGPSVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 239 EPKSCDKHTHTCPCPAPELLGGPSVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 298  
QY 61 NMVYDGEVHNKTKPREEQYNSTRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
DB 239 NMVYDGEVHNKTKPREEQYNSTRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 358  
QY 121 ISKAVQPREPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGOPENNYKTP 180  
DB 359 ISKAVQPREPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGOPENNYKTP 418  
QY 181 PVLDSGSEFFLYSKLTVDKSRWQGNVFCSVMEALHNHYOQRLSLSPGK 232  
DB 419 PVLDSGSEFFLYSKLTVDKSRWQGNVFCSVMEALHNHYOQRLSLSPGK 470

## RESULT 7

Q6N089 PRELIMINARY; PRT; 472 AA.

ID Q6N089  
AC Q6N089;  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DE Hypothetical protein DKFZp686p15220.  
GN Name=DKFZp686p15220;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RG The German Human cDNA Consortium;  
RA Wambut R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BK640627; CAB45781.1; -.

DR HSP; F01861; IADQ.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG v.  
DR Pfam; PF07654; Cl-set: 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 472;  
Best Local Similarity 97.0%; Pred. No. 2.8e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPELLGGPSVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 60

```

Db      241  |||||
EPKSCDKHTHTCPCPAPBLGGPSVFLPPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 300
Qy      61  NWYDGEVHNVKTKPREEQYNSTYRVSVLTVLHQNMMNGKEYCKVSNKLPAPIEKT 120
Db      301  NWYDGEVHNAKTKPREEQYNSTYRVSVLTVLHQNMMNGKEYCKVSNKLPAPIEKT 360
Qy      121  ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTP 180
Db      361  ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTP 420
Qy      181  PVLDSGSEFFLYSKLTVDKSRMQQGNVSCSVMEHALNHNHQQRSLSPGK 232
Db      421  PVLDSGSEFFLYSKLTVDKSRMQQGNVSCSVMEHALNHNHQQRSLSPGK 472

RESULT 8
O6GMW7  PRELIMINARY; PRT; 475 AA.
AC  O6GMW7  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
OS  Hypothetical protein.
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN  NCBI_TaxID=9606;
RP  SEQUENCE FROM N.A.
RC  TISSUE=Spleen;
RX  MEDLINE=22288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Datchenko L., Murnusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Useth T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Krzyszinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Spleen;
RA  Strausberg R.;
RL  Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC073782; AAH73782.1; -.
DR  InterPro; IPR003599; IG.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003597; IG.cl.
DR  InterPro; IPR003006; IG_MHC.
DR  Pfam; PF07654; CI-secl; 3.
DR  Pfam; PF00047; IG; 4.
DR  SMART; SM00409; IG; 2.
DR  SMART; SM00407; IGcl; 3.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 4.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KV  Hypothetical protein.
SQ  SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;

```

```

Query Match      97.2% Score 1225; DB 2; Length 475;
Beet Local Similarity 97.0%; Pred. No.2.8e-88;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1  EPKSCDKHTHTCPCPAPBLGGPSVFLPPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 60
Db      244  EPKSCDKHTHTCPCPAPBLGGPSVFLPPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 303
Qy      61  NWYDGEVHNVKTKPREEQYNSTYRVSVLTVLHQNMMNGKEYCKVSNKLPAPIEKT 120
Db      304  NWYDGEVHNAKTKPREEQYNSTYRVSVLTVLHQNMMNGKEYCKVSNKLPAPIEKT 363
Qy      121  ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTP 180
Db      364  ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTP 423
Qy      181  PVLDSGSEFFLYSKLTVDKSRMQQGNVSCSVMEHALNHNHQQRSLSPGK 232
Db      424  PVLDSGSEFFLYSKLTVDKSRMQQGNVSCSVMEHALNHNHQQRSLSPGK 475

RESULT 9
O6GMX1  PRELIMINARY; PRT; 476 AA.
AC  O6GMX1  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
OS  Hypothetical protein.
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN  NCBI_TaxID=9606;
RP  SEQUENCE FROM N.A.
RC  TISSUE=Spleen;
RX  MEDLINE=22288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Datchenko L., Murnusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Useth T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Krzyszinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Spleen;
RA  Strausberg R.;
RL  Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC073773; AAH73773.1; -.
DR  InterPro; IPR003599; IG.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003597; IG.cl.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003596; IG-secl; 3.
DR  Pfam; PF07654; CI-secl; 3.
DR  Pfam; PF00047; IG; 4.
DR  SMART; SM00409; IG; 2.
DR  SMART; SM00407; IGcl; 3.
DR  SMART; SM00406; IGV; 1.

```

DR PROSITE: PS50835; IG\_LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 476 AA; 52286 MW; 622ABA5C6ZDDE9D CRC64;  
Query Match 97.2%; Score 1225; DB 2; Length 476;  
Best Local Similarity 97.0%; Pred. No. 2.8e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 60  
DB 245 EPKSCDKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 304  
QY 61 NMYVDGVEVHNAKTKRREEQNSTYRVSVLTLYHQNMNGEKYCKKVSNNKALPAPIEKT 120  
DB 305 NMYVDGVEVHNAKTKRREEQNSTYRVSVLTLYHQNMNGEKYCKKVSNNKALPAPIEKT 364  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGOPENNYKTT 180  
DB 365 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGOPENNYKTT 424  
QY 181 PVLDSVGSFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYOQKSLSLSPGK 232  
DB 425 PVLDSVGSFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYOQKSLSLSPGK 476  
RESULT 10  
ID 096P08 PRELIMINARY; PRT; 679 AA.  
AC 096P08;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Factor VII active site mutant immunocjugate.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;  
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor  
cells for immunotherapy in mouse models of prostatic cancer."  
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).  
[2]  
RA Hu Z., Garen A.,  
RP Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AF272774; AAK58686.2; -.  
DR HSSP; P08709; 1KLI.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000152; Asx hydroxyl\_S.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001821; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_Like.  
DR InterPro; IPR007110; IG\_c1.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR InterPro; IPR000294; Vitk\_dep\_Glu.  
DR Pfam; PF07654; Cl-sec; 2.  
DR Pfam; PF00008; EGF\_1.  
DR Pfam; PF00594; GlA; 1.  
DR Pfam; PF00089; Trypsin; 1.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00069; GlA; 1.  
DR SMART; SM00407; IGc1; 1.

DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE: PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE: PS01186; EGF\_2; 1.  
DR PROSITE: PS50026; EGF\_3; 1.  
DR PROSITE: PS01187; EGF\_CA; 1.  
DR PROSITE: PS00011; GlA\_1; 1.  
DR PROSITE: PS50835; IG\_LIKE; 2.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
KW EGF-like domain; Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;  
Query Match 97.2%; Score 1225; DB 2; Length 679;  
Best Local Similarity 97.0%; Pred. No. 4.3e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 60  
DB 448 EPKSCDKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 507  
QY 61 NMYVDGVEVHNAKTKRREEQNSTYRVSVLTLYHQNMNGEKYCKKVSNNKALPAPIEKT 120  
DB 508 NMYVDGVEVHNAKTKRREEQNSTYRVSVLTLYHQNMNGEKYCKKVSNNKALPAPIEKT 567  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGOPENNYKTT 180  
DB 568 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGOPENNYKTT 627  
QY 181 PVLDSVGSFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYOQKSLSLSPGK 232  
DB 628 PVLDSVGSFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYOQKSLSLSPGK 679  
RESULT 11  
ID 06P055 PRELIMINARY; PRT; 473 AA.  
AC 06P055;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Peridheral Nervous System;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko I., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stacheron M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.D., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
RA Whaley J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]

```
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strussberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH65820.1; -.
DR HSSP; P01661; IADO.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129857 CRC64;

Query Match          96.9%; Score 1221; DB 2; Length 473;
Best Local Similarity 96.6%; Pred. No. 5,8e-88;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 242 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 301
QY 61 NMYVDGVEVHANKTPREEOYNSTRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
DB 302 NMYVDGVEVHANKTPREEOYNSTRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 361
QY 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 180
DB 362 ISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 421
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMEHALHNHYQOQSLSLSPGK 232
DB 422 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMEHALHNHYQOQSLSLSPGK 473

RESULT 12
Q6MZ06 PRELIMINARY; PRT; 475 AA.
AC Q6MZ06;
DR 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp666G11190.
OS Homo sapiens (Human).
GN Name=DKFZp666G11190;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RA The German Human cDNA Consortium;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -.
DR HSSP; P01661; IADO.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;

Query Match          96.9%; Score 1221; DB 2; Length 480;
Best Local Similarity 96.6%; Pred. No. 5,9e-88;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
```

```
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match          96.9%; Score 1221; DB 2; Length 475;
Best Local Similarity 96.6%; Pred. No. 5,8e-88;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 244 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 303
QY 61 NMYVDGVEVHANKTPREEOYNSTRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
DB 304 NMYVDGVEVHANKTPREEOYNSTRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 363
QY 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 180
DB 364 ISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 423
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMEHALHNHYQOQSLSLSPGK 232
DB 424 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMEHALHNHYQOQSLSLSPGK 475

RESULT 13
Q6N094 PRELIMINARY; PRT; 480 AA.
AC Q6N094;
DR 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp666O01196.
GN Name=DKFZp666O01196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RA The German Human cDNA Consortium;
RA Wandut R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640622; CAE45776.1; -.
DR HSSP; P01661; IADO.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;

Query Match          96.9%; Score 1221; DB 2; Length 480;
Best Local Similarity 96.6%; Pred. No. 5,9e-88;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
```

QY 121 ISKAVQREPOVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 180  
DB 369 ISKAGQPREPOVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 428  
QY 181 PVLDSVGSFELYSKLTVDKSRWQGNVFSQVMEHALNHHYQORSLSLSPGK 232  
DB 429 PVLDSVGSFELYSKLTVDKSRWQGNVFSQVMEHALNHHYQORSLSLSPGK 480

## RESULT 14

Q6N097 PRELIMINARY; PRT; 481 AA.  
AC Q6N097;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686H20196.  
GN Name=DKFZp686H20196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human esophagus tumor;  
RA The German Human CDNA Consortium;  
RA Mambut R., Heuber D., Mewes H.W., Weil B., Amid C., Oanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BX640619; CAE45773.1; -.  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-1like.  
DR InterPro; IPR003597; IG-1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IG1; 3.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
DR Hypothetical protein.  
KW SEQUENCE 481 AA; 52759 MW; 47220D9E64BDF98B CRC64;  
SQ  
Query Match 96.9%; Score 1221; DB 2; Length 481;  
Best Local Similarity 96.6%; Pred. No. 5.9e-88;  
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTHTCPCPAPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 250 EPKSCDKHTHTCPCPAPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 309  
QY 61 NMYVDGVEVHNAKTPREBOYNSTYRVSVLTFLHQMNGKEYCKVSNKALPAPIEKT 120  
DB 310 NMYVDGVEVHNAKTPREBOYNSTYRVSVLTFLHQMNGKEYCKVSNKALPAPIEKT 369  
QY 121 ISKAVQPREPOVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 180  
DB 370 ISKAGQPREPOVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 429  
QY 181 PVLDSVGSFELYSKLTVDKSRWQGNVFSQVMEHALNHHYQORSLSLSPGK 232  
DB 430 PVLDSVGSFELYSKLTVDKSRWQGNVFSQVMEHALNHHYQORSLSLSPGK 481

## RESULT 15

Q72351 PRELIMINARY; PRT; 482 AA.  
AC Q72351;  
DT 01-OCT-2003 (TREMBlrel. 25, Created)  
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Hypothetical protein DKFZp686N02209.  
GN Name=DKFZp686N02209;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Oanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BX538118; CAD98026.1; -.  
DR HSSP; P01857; IGH.  
DR InterPro; IPR007110; IG-1like.  
DR InterPro; IPR003597; IG-1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein  
SQ SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;  
QY 1 EPKSCDKHTHTCPCPAPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 251 EPKSCDKHTHTCPCPAPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 310  
QY 61 NMYVDGVEVHNAKTPREBOYNSTYRVSVLTFLHQMNGKEYCKVSNKALPAPIEKT 120  
DB 311 NMYVDGVEVHNAKTPREBOYNSTYRVSVLTFLHQMNGKEYCKVSNKALPAPIEKT 370  
QY 121 ISKAVQPREPOVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 180  
DB 371 ISKAGQPREPOVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 430  
QY 181 PVLDSVGSFELYSKLTVDKSRWQGNVFSQVMEHALNHHYQORSLSLSPGK 232  
DB 431 PVLDSVGSFELYSKLTVDKSRWQGNVFSQVMEHALNHHYQORSLSLSPGK 482

Search completed: June 7, 2005, 09:01:28  
Job time : 115.197 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 08:38:56 ; Search time 117.803 Seconds  
(without alignments)  
761.681 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260  
Sequence: 1 EPKSCDKHTKCPKPAPLL.....MHEALNHYQGRSLSPGK 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: \_Geneseq\_16Dec04:\*  
2: geneseqp1980s:\*  
3: geneseqp1990s:\*  
4: geneseqp2000s:\*  
5: geneseqp2001s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1260	100.0	232	6	AAO19665 Human IgG
2	1260	100.0	330	6	AAO19664 Human IgG
3	1260	100.0	569	6	AAO19668 GR2 fusio
4	1225	97.2	232	2	AAW26232 Human IgG
5	1225	97.2	232	3	AAW26232 Human IgG
6	1225	97.2	232	4	AAW26232 Human IgG
7	1225	97.2	232	4	AAW26232 Human IgG
8	1225	97.2	232	4	AAW26232 Human IgG
9	1225	97.2	232	5	AAW26232 Human IgG
10	1225	97.2	232	7	ADJ65991 Herpes vi
11	1225	97.2	232	8	ADJ65991 Herpes vi
12	1225	97.2	232	8	ADJ65991 Herpes vi
13	1225	97.2	232	8	ADJ65991 Herpes vi
14	1225	97.2	232	8	ADJ65991 Herpes vi
15	1225	97.2	232	8	ADJ65991 Herpes vi
16	1225	97.2	232	8	ADJ65991 Herpes vi
17	1225	97.2	232	8	ADJ65991 Herpes vi
18	1225	97.2	232	8	ADJ65991 Herpes vi
19	1225	97.2	232	8	ADJ65991 Herpes vi
20	1225	97.2	232	8	ADJ65991 Herpes vi
21	1225	97.2	232	8	ADJ65991 Herpes vi
22	1225	97.2	232	8	ADJ65991 Herpes vi
23	1225	97.2	232	8	ADJ65991 Herpes vi
24	1225	97.2	232	8	ADJ65991 Herpes vi
25	1225	97.2	232	8	ADJ65991 Herpes vi

26	1225	97.2	329	8	ADP56389 Human PRO
27	1225	97.2	329	8	ADP56389 Human PRO
28	1225	97.2	330	4	AAO19665 standard; protein; 232 AA.
29	1225	97.2	330	5	AAW26232 Human IgG
30	1225	97.2	330	5	AAW26232 Human IgG
31	1225	97.2	330	5	AAW26232 Human IgG
32	1225	97.2	330	5	AAW26232 Human IgG
33	1225	97.2	330	6	AAW26232 Human IgG
34	1225	97.2	330	6	AAW26232 Human IgG
35	1225	97.2	330	6	AAW26232 Human IgG
36	1225	97.2	330	6	AAW26232 Human IgG
37	1225	97.2	330	6	AAW26232 Human IgG
38	1225	97.2	330	6	AAW26232 Human IgG
39	1225	97.2	330	6	AAW26232 Human IgG
40	1225	97.2	330	6	AAW26232 Human IgG
41	1225	97.2	330	7	ADP56389 Human PRO
42	1225	97.2	330	7	ADP56389 Human PRO
43	1225	97.2	330	7	ADP56389 Human PRO
44	1225	97.2	330	8	ADP56389 Human PRO
45	1225	97.2	330	8	ADP56389 Human PRO

ALIGNMENTS

RESULT 1  
AAO19665  
ID AAO19665 standard; protein; 232 AA.  
XX  
AC AAO19665;  
DT 28-MAR-2003 (first entry)  
DE Human IgG1 heavy chain constant region hinge-CH2-CH3 portion.  
KW Human; IgG1; immunoglobulin G; immunotherapy; immune disease;  
KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;  
KW antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic;  
KW antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic;  
KW hinge-CH2-CH3 region.  
OS Homo sapiens.  
PN WO200288317-A2.  
PD 07-NOV-2002.  
XX  
PF 01-MAY-2002; 2002WO-US013527.  
XX  
PR 01-MAY-2001; 2001US-00847208.  
PR 24-OCT-2001; 2001US-0000439.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Saxon A, Zhang K, Zhu D;  
XX  
DR WPI; 2003-103456/09.  
XX  
PT New fusion molecules comprising polypeptide sequences that bind to IgG  
PT inhibitory receptor and native IgG receptor, useful for treating IgE-  
PT mediated hypersensitivity reactions, e.g. asthma or allergies, or  
PT autoimmune diseases.  
PS Claim 19; Fig 3; 116pp; English.  
XX  
CC The present invention relates to a fusion molecule comprising a first  
CC polypeptide sequence capable of specific binding to a native IgG  
CC inhibitory receptor consisting of an immune receptor tyrosine-based  
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
CC functionally connected to a second polypeptide sequence capable of  
CC specific binding directly or indirectly to a native IgG receptor  
CC (Fc epsilonR). Also provided are nucleotide sequences encoding such a  
CC fusion protein. The fusion molecules and compositions are useful for



CC treating an IGE-mediated biological response, preferably an IGE-mediated  
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,  
CC or symptoms resulting from, a type I hypersensitivity reaction in a  
CC subject receiving immunotherapy. The present sequence is the human IgG1  
CC heavy chain constant region hinge-CH2-CH3 portion  
XX  
SQ Sequence 232 AA;  
Query Match 100.0%; Score 1260; DB 6; Length 232;  
Best Local Similarity 100.0%; Pred. No. 2.9e-91;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTHTCPCPAPELLGSPSVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPELLGSPSVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMYVDGVEVHNVKTRREQYNSTRVVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120  
DB 61 NMYVDGVEVHNVKTRREQYNSTRVVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120  
QY 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
DB 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVSCSYMEALHNHYQORSLSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVSCSYMEALHNHYQORSLSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVSCSYMEALHNHYQORSLSLSPGK 232  
RESULT 2  
ID AAO19664 standard; protein; 330 AA.  
XX AAO19664;  
XX  
XX 28-MAR-2003 (first entry)  
XX  
DE Human IgG1 heavy chain constant region.  
XX  
XX Human; IgG1; immunoglobulin G; immunotherapy; immune disease;  
KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;  
KW antiaesthetic; antiallergic; antiinflammatory; dermatological;  
XX antiasthmatic; antineumatic; antidiabetic; neuroprotective.  
XX  
OS Homo sapiens.  
XX  
PN WO200288317-A2.  
XX  
PD 07-NOV-2002.  
XX  
PF 01-MAY-2002; 2002WO-US013527.  
XX  
PR 01-MAY-2001; 2001US-00847208.  
XX  
PR 24-OCT-2001; 2001US-00000439.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Saxon A, Zhang K, Zhu D;  
XX  
XX WPI; 2003-103456/09.  
XX  
XX New fusion molecules comprising polypeptide sequences that bind to IgG  
XX inhibitory receptor and native IGF receptor, useful for treating IGF-  
XX mediated hypersensitivity reactions, e.g. asthma or allergies, or  
XX autoimmune diseases.  
XX  
XX Claim 64; Fig 2; 116pp; English.  
XX  
XX The present invention relates to a fusion molecule comprising a first  
XX polypeptide sequence capable of specific binding to a native IGF

CC inhibitory receptor consisting of an immune receptor tyrosine-based  
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
CC functionally connected to a second polypeptide sequence capable of  
CC specific binding directly or indirectly to a native IGF receptor  
CC (Fc epsilon1). Also provided are nucleotide sequences encoding such a  
CC fusion protein. The fusion molecules and compositions are useful for  
CC treating an IGE-mediated biological response, preferably an IGE-mediated  
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,  
CC or symptoms resulting from, a type I hypersensitivity reaction in a  
CC subject receiving immunotherapy. The present sequence is the human IgG1  
CC heavy chain constant region  
XX  
SQ Sequence 330 AA;  
Query Match 100.0%; Score 1260; DB 6; Length 330;  
Best Local Similarity 100.0%; Pred. No. 4.4e-91;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTHTCPCPAPELLGSPSVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 99 EPKSCDKHTHTCPCPAPELLGSPSVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 158  
QY 61 NMYVDGVEVHNVKTRREQYNSTRVVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120  
DB 61 NMYVDGVEVHNVKTRREQYNSTRVVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 218  
QY 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
DB 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 278  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVSCSYMEALHNHYQORSLSLSPGK 232  
DB 279 PVLDSVGSFFLYSKLTVDKSRWQGNVSCSYMEALHNHYQORSLSLSPGK 330  
RESULT 3  
ID AAO19668 standard; protein; 569 AA.  
XX AAO19668;  
XX  
XX 28-MAR-2003 (first entry)  
XX  
DE GE2 fusion protein for use in treating immune diseases.  
XX  
XX Human; IGE; immunoglobulin E; immunotherapy; immune disease;  
KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;  
KW antiaesthetic; antiallergic; antiinflammatory; dermatological; GE2;  
XX antiasthmatic; antineumatic; antidiabetic; neuroprotective;  
XX fusion protein.  
XX  
OS Synthetic.  
XX  
OS Unidentified.  
XX  
PN WO200288317-A2.  
XX  
PD 07-NOV-2002.  
XX  
PF 01-MAY-2002; 2002WO-US013527.  
XX  
PR 01-MAY-2001; 2001US-00847208.  
XX  
PR 24-OCT-2001; 2001US-00000439.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Saxon A, Zhang K, Zhu D;  
XX  
XX WPI; 2003-103456/09.  
XX  
XX New fusion molecules comprising polypeptide sequences that bind to IGF

PT inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.

Claim 35; Fig 7; 116pp; English.

CC The present invention relates to a fusion molecule comprising a first  
CC polypeptide sequence capable of specific binding to a native IgE  
CC inhibitory receptor consisting of an immune receptor tyrosine-based  
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
CC functionally connected to a second polypeptide sequence capable of  
CC specific binding directly or indirectly to a native IgE receptor  
CC (Fcεpsilon1). Also provided are nucleotide sequences encoding such a  
CC fusion protein. The fusion molecules and compositions are useful for  
CC creating an IgE-mediated biological response, preferably an IgE-mediated  
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
CC anaphylactic shock, or autoimmune diseases such as rheumatoid arthritis,  
CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,  
CC or symptoms resulting from, a type I hypersensitivity reaction in a  
CC subject receiving immunotherapy. The present sequence is a gammahinge-  
CC CChgammam2-Chgammam3-(Gly4Ser)3-Chepsilon1on2-Chepsilon1on3-Chepsilon1on3 fusion  
CC protein (designated GE2) of the invention

SQ Sequence 569 AA;

Query Match 100.0%; Score 1260; DB 6; Length 569;

Best Local Similarity 100.0%; Pred. No. 8.5e-91; Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMTSRTEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMTSRTEVTCVVVDVSHEDPEVKF 60  
QY 61 NMVYDGEVHANKTPREBQVNSTYRVSVLTVLHQDNMNGKEKKCKVSNKALPAPIETK 120  
DB 61 NMVYDGEVHANKTPREBQVNSTYRVSVLTVLHQDNMNGKEKKCKVSNKALPAPIETK 120  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 180  
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSYVMEALAHNHYOQRSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSYVMEALAHNHYOQRSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSYVMEALAHNHYOQRSLSPGK 232

RESULT 4

AAW26232

ID AAW26232 standard; protein; 232 AA.

AC AAW26232;

DT 16-MAR-1998 (first entry)

DE Human IgG1 hinge/Fc region.

KW Fusion protein; hydrophilic spacer; recombinant; expression system;  
KW carboxypeptidase; IgG1; immunoglobulin; hinge region; Fc.

OS Homo sapiens.

PN WO9728272-A1.

PD 07-AUG-1997.

PF 31-JAN-1997; 97WO-US001470.

PR 31-JAN-1996; 96US-00595043.

XX (TECH-) TECHNOLOGENE INC.

PI Sgarlato CD;

XX WPI; 1997-402624/37.  
DR N-PSDB; AAT80158.

PT Recombinant protein expression system for fusion protein production -  
PT useful for high quantity production of authentic recombinant proteins.

PS Example 3; Page 133-134; 194pp; English.

CC A novel recombinant vector has been developed which comprises a  
CC nucleotide sequence encoding a fusion protein. The fusion protein  
CC comprises three domains joined together in order, from N-terminus to C-  
CC terminus, of a first domain comprising a protein of interest, a second  
CC domain comprising a hydrophilic spacer and an affinity domain, each  
CC domain comprising amino acid residues. The present sequence represents  
CC the hinge/Fc region of human IgG1, used in example 3 of the present  
CC invention. The recombinant vector is used for the production of authentic  
CC recombinant proteins of interest. The method of the invention is useful  
CC for the expression of fusion proteins capable of isolation by affinity  
CC chromatography in pro- or eukaryotic cells. This method allows for the  
CC efficient cleavage and generation of authentic proteins of interest that  
CC do not contain extraneous (i.e. non-naturally occurring) amino acids

SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 2; Length 232;

Best Local Similarity 97.0%; Pred. No. 1.7e-88; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMTSRTEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMTSRTEVTCVVVDVSHEDPEVKF 60  
QY 61 NMVYDGEVHANKTPREBQVNSTYRVSVLTVLHQDNMNGKEKKCKVSNKALPAPIETK 120  
DB 61 NMVYDGEVHANKTPREBQVNSTYRVSVLTVLHQDNMNGKEKKCKVSNKALPAPIETK 120  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 180  
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSYVMEALAHNHYOQRSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSYVMEALAHNHYOQRSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSYVMEALAHNHYOQRSLSPGK 232

RESULT 5

AAB28690

ID AAB28690 standard; protein; 232 AA.

AC AAB28690;

DT 14-FEB-2001 (first entry)

DE Human IgGammal hinge, CH2 and CH3 regions.

KW Human; ACP-1; type II transmembrane protein; cytosolic; antiviral;  
KW antinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;  
KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;  
KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;  
KW transplant rejection; cardiovascular disease; arteriosclerosis;  
KW IgGammal.

OS Homo sapiens.

PN WO200063253-A1.

PD 26-OCT-2000.

PF 24-MAR-2000; 2000WO-US008004.

PR 16-APR-1999; 99US-00293245.

XX Sgarlato CD;

PA (AMGE-) AMGEN INC.  
XX Hsu H, Meng S;  
XX WPI; 2000-665240/64.  
XX Fusion protein of AGP-1 protein and an Fc region, used to treat  
PT proliferative disorders, immune disorders, and virally-induced disorders.  
XX  
XX Claim 2; Fig 1; 93pp; English.  
XX  
XX The present sequence was used in the production of AGP-1 fusion proteins.  
CC AGP-1 is a type II transmembrane protein. The fusion proteins comprise an  
CC Fc immunoglobulin region fused to the N-terminal portion of the AGP-1  
CC protein. The fusion proteins can be used to induce apoptosis in a tissue,  
CC and to treat proliferative disorders, immune disorders, or virally-  
CC induced disorders. The proliferative disorders include cancers, such as  
CC breast, prostate, lung or colon cancer. The viral infections include  
CC hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune  
CC disorders may be autoimmune disorders or transplant rejection.  
CC Cardiovascular diseases such as arteriosclerosis may also be treated. The  
CC AGP-1 containing fusion proteins have increased biological activity  
CC compared to the soluble AGP-1 proteins used in prior art therapies  
XX  
XX Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 3; Length 232;  
Best Local Similarity 97.0%; Pred. No. 1.7e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NWYVDGVEVHNAKTKRREQYSTYRVSVLTGLVHQMNGKEYCKYCNKALPAPIEKT 120  
DB 61 NWYVDGVEVHNAKTKRREQYSTYRVSVLTGLVHQMNGKEYCKYCNKALPAPIEKT 120  
QY 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVMEESNGQPENNYKTTT 180  
DB 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVMEESNGQPENNYKTTT 180  
QY 181 PVLDSVGSFPLYSKLTVDKSRWQGQNVFSCSYMHEALHNHYTQKSLSLSPGK 232  
DB 181 PVLDSVGSFPLYSKLTVDKSRWQGQNVFSCSYMHEALHNHYTQKSLSLSPGK 232

RESULT 6  
AAB80897  
ID AAB80897 standard; protein; 232 AA.  
XX  
XX AAB80897;  
XX  
XX 31-MAY-2001 (first entry)  
XX  
XX Human IgGammal hinge, CH2 and CH3 regions.  
XX  
XX Human; IgGammal; anticancer; Antimetastatic; Osteogenic;  
XX  
XX lytic bone disease; multiple myeloma; immunoglobulin;  
XX  
XX osteoclast bone metastasis; OPG; osteoprotegerin;  
XX  
XX osteoclast formation inhibition; bone resorption inhibition.  
XX  
XX Homo sapiens.  
XX  
XX WO200117543-A2.  
XX  
XX 15-MAR-2001.  
XX  
XX 18-AUG-2000; 2000WO-US022806.  
XX  
XX 03-SEP-1999; 99US-00389545.  
XX  
XX (AMGE-) AMGEN INC.  
PA

XX Dunstan CR;  
XX WPI; 2001-265936/27.  
XX  
XX Preventing or treating lytic bone diseases, particularly associated with  
PT cancer or metastasis, by administering an osteoprotegerin polypeptide.  
XX  
XX Disclosure; Fig 1; 87pp; English.  
XX  
XX

CC The present invention relates to a method for the prevention or treatment  
CC of lytic bone disease or multiple myeloma. Also the method can be used  
CC for preventing metastasis of cancer to bone or osteoclast bone  
CC metastasis. The method comprises administering an OPG (osteoprotegerin)  
CC polypeptide or OPG fusion protein. The OPG proteins (see AAB80898-  
CC AAB80905) can inhibit formation of osteoclasts (and thus bone resorption)  
CC by blocking differentiation from monocytes/macrophage precursors. The  
CC present sequence is the hinge, CH2 and CH3 regions of human IgGammal.  
CC This sequence can be used to generate fusion proteins of OPG and  
CC immunoglobulin, for use in the present invention. The generated fusion  
CC proteins can exhibit increased circulating half-lives and slower  
CC clearance times, thereby providing a more sustained activity  
XX  
XX Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 4; Length 232;  
Best Local Similarity 97.0%; Pred. No. 1.7e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NWYVDGVEVHNAKTKRREQYSTYRVSVLTGLVHQMNGKEYCKYCNKALPAPIEKT 120  
DB 61 NWYVDGVEVHNAKTKRREQYSTYRVSVLTGLVHQMNGKEYCKYCNKALPAPIEKT 120  
QY 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVMEESNGQPENNYKTTT 180  
DB 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVMEESNGQPENNYKTTT 180  
QY 181 PVLDSVGSFPLYSKLTVDKSRWQGQNVFSCSYMHEALHNHYTQKSLSLSPGK 232  
DB 181 PVLDSVGSFPLYSKLTVDKSRWQGQNVFSCSYMHEALHNHYTQKSLSLSPGK 232

RESULT 7  
AAV72915  
ID AAV72915 standard; protein; 232 AA.  
XX  
XX AAV72915;  
XX  
XX 13-JUN-2001 (first entry)  
XX  
XX Human partial IgG1 protein comprising hinge, CH2 and CH3 regions.  
XX  
XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;  
XX  
XX therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;  
XX  
XX hypercalcemia; osteopenia; osteonecrosis; rheumatoid arthritis;  
XX  
XX osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;  
XX  
XX periodontal.  
XX  
XX Homo sapiens.  
XX  
XX WO200118203-A1.  
XX  
XX 15-MAR-2001.  
XX  
XX 18-AUG-2000; 2000WO-US022797.  
XX  
XX 03-SEP-1999; 99US-00389782.  
XX  
XX (AMGE-) AMGEN INC.  
PA

XX Dunstan CR, Wooden SK, Mann MB;  
XX  
XX WPI; 2001-244572/25.  
XX  
XX Osteoprotegerin-Fc protein fusions useful for treating bone loss caused  
XX by e.g. osteoporosis, Paget's disease and osteomyelitis.  
XX  
XX Claim 3; Fig 1; 119pp; English.  
XX  
XX The patent discloses fusion protein comprising human osteoprotegerin  
XX (OPG) protein fused by linker to human IgG1 Fc portion. OPG negatively  
XX regulates formation of osteoclasts in vitro and in vivo. It blocks the  
XX differentiation of osteoclasts from monocyte or macrophage precursors and  
XX the reabsorption of bone. The OPG-Fc fusion protein is administered for  
XX the treatment of bone loss resulting from osteoporosis, Paget's disease,  
XX osteomyelitis, hypercalcaemia, osteopenia associated with surgery or  
XX steroid administration, osteonecrosis, bone loss due to rheumatoid  
XX arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic  
XX loosening. The present sequence is partial human immunoglobulin G (Ig G)  
XX C1 protein comprising the hinge and heavy chain constant regions CH2 and  
XX CH3  
SQ Sequence 232 AA;  
Query Match 97.2%; Score 1225; DB 4; Length 232;  
Best Local Similarity 97.0%; Pred. No. 1.7e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTHTCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMYVGVGVHNAKTKRREQVNSTYRVSVLTVLIQDMNMGKEYCKCKVSNKALPAPIEKT 120  
DB 61 NMYVGVGVHNAKTKRREQVNSTYRVSVLTVLIQDMNMGKEYCKCKVSNKALPAPIEKT 120  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
QY 181 PVLDSVGSFFLYSKLTVDSKRWQOGNVFSCSVMEALHNHYQKSLSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDSKRWQOGNVFSCSVMEALHNHYQKSLSLSPGK 232  
RESULT 8  
AAE15347 standard; protein; 232 AA.  
ID AAE15347;  
AC AAE15347;  
XX  
XX 09-APR-2002 (first entry)  
XX  
XX Human immunoglobulin G (IgG) gamma 1 constant heavy chain hinge region.  
XX  
XX Human; erythropoietin; Epo; haematocrit; anaemia; kidney function; IgG;  
XX cancer; myeloid suppressive therapy; anti-viral drug; immunoglobulin G.  
XX  
XX Homo sapiens.  
XX  
XX WO200181405-A2.  
XX  
XX PN  
XX 01-NOV-2001.  
XX  
XX PD  
XX 19-APR-2001; 2001WO-US012836.  
XX  
XX PF  
XX 21-APR-2000; 2000US-00559001.  
XX  
XX PR  
XX (AMGE-) AMGEN INC.  
XX  
XX PA  
XX Egrle JC, Elliott SG, Browne JK, Sitney KC;  
XX  
XX

DR WPI; 2002-034433/04.  
XX  
XX Increasing and maintaining haematocrit in mammal suffering from anemia,  
XX comprising administering hyperglycosylated analog of erythropoietin less  
XX frequently and at lower molar amount of recombinant human erythropoietin.  
XX  
XX Example 1; Fig 10; 95pp; English.  
XX  
XX The invention relates to a method for increasing and maintaining  
XX haematocrit in a mammal. The method comprises administering a  
XX hyperglycosylated analogue of erythropoietin (Epo) in a pharmaceutical  
XX composition, less frequently than an equivalent molar amount of and at a  
XX lower molar amount than recombinant human Epo (rHuEpo) to obtain a  
XX comparable target haematocrit. Epo is a glycoprotein hormone necessary  
XX for the maturation of erythroid progenitor cells into erythrocytes. Human  
XX Epo analogue is useful for raising and maintaining haematocrit to a  
XX comparable target haematocrit in a mammal suffering from anaemia  
XX associated with a decline or loss of kidney function, myelosuppressive  
XX therapy comprising chemotherapeutic or anti-viral drugs or associated  
XX with excessive blood loss during surgical procedures, and in cancer  
XX condition. The present sequence is human immunoglobulin G (IgG) gamma 1  
XX constant heavy chain (CH2, CH3) hinge region used to construct Epo  
XX hyperglycosylated analogue fusion protein  
SQ Sequence 232 AA;  
Query Match 97.2%; Score 1225; DB 5; Length 232;  
Best Local Similarity 97.0%; Pred. No. 1.7e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTHTCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMYVGVGVHNAKTKRREQVNSTYRVSVLTVLIQDMNMGKEYCKCKVSNKALPAPIEKT 120  
DB 61 NMYVGVGVHNAKTKRREQVNSTYRVSVLTVLIQDMNMGKEYCKCKVSNKALPAPIEKT 120  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
QY 181 PVLDSVGSFFLYSKLTVDSKRWQOGNVFSCSVMEALHNHYQKSLSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDSKRWQOGNVFSCSVMEALHNHYQKSLSLSPGK 232  
RESULT 9  
AAE26272 standard; protein; 232 AA.  
ID AAE26272;  
AC AAE26272;  
XX  
XX 14-NOV-2002 (first entry)  
XX  
XX Human IgG1 heavy chain.  
XX  
XX Human; amyloidogenic protein; Alzheimer's disease; Huntington's disease;  
XX spongiform encephalopathy; familial amyloid cardiomyopathy; amyloidosis;  
XX Gerstmann-Strausler-Scheinker syndrome; spongiform encephalopathy; GSS;  
XX Creutzfeldt-Jacob disease; insulinoma; diabetes; body myocytis; myeloma;  
XX CJ.  
XX  
XX XX  
XX Homo sapiens.  
XX  
XX OS  
XX WO200242462-A2.  
XX  
XX PN  
XX 30-MAY-2002.  
XX  
XX PD  
XX 27-NOV-2001; 2001WO-US044581.  
XX  
XX PF  
XX 27-NOV-2000; 2000US-0253302P.  
XX  
XX PR  
XX 29-NOV-2000; 2000US-0250198P.  
XX  
XX

PR 20-DEC-2000; 2000US-0257186P.  
XX (PRAE-) PRAECIS PHARM INC.  
XX  
XX  
PI Gelfer ML, Ierael DI, Joyal JL, Gosselin M;  
XX MPI; 2002-636427/68.  
XX  
PT Novel therapeutic agent useful for treating an amyloidogenic disorder,  
XX e.g. Alzheimer's disease, comprises an immunoglobulin heavy chain  
XX constant region linked to a peptide capable of binding amyloidogenic  
XX protein.

PS Example 8; Page 76; 79pp; English.

CC The invention relates to a compound comprising an immunoglobulin (Ig)  
CC heavy chain constant region or its fragment that retains the ability to  
CC bind an Fc receptor linked by a linker group or a direct bond to a  
CC peptide capable of binding an amyloidogenic protein. The invention is  
CC useful for clearing an amyloidogenic protein such as beta-amyloid,  
CC transthyretin (TTR), prion protein (PrP), islet amyloid polypeptide  
CC (IAPP), atrial natriuretic factor (ANF), kappa light chain, lambda light  
CC chain, amyloid A, procalcitonin, cystatin C, beta2-microglobulin, ApoA-I,  
CC gelsolin, calcitonin, fibrinogen, Huntingtin, alpha-synuclein and  
CC lysozyme from a subject and for treating an amyloidogenic disorder such  
CC as Alzheimer's disease and spongiform encephalopathy. Disorders treatable  
CC include those caused or characterised by deposits of TTR (eg. familial  
CC amyloid cardiomyopathy), PrP (eg. spongiform encephalopathies, including  
CC scrapie in sheep, bovine spongiform encephalopathy in cows and  
CC Creutzfeldt-Jacob disease (CJ) and Gerstmann-Strausler-Scheinker  
CC syndrome (GSS) in humans), IAPP (eg. insulinoma, adult onset diabetes),  
CC ANF (eg. isolated atrial amyloid), kappa or lambda light chain (eg.  
CC idiopathic amyloidosis, myeloma), amyloid A (eg. amyloidosis), Apo A-I  
CC (eg. hereditary non-neuropathic systemic amyloidosis), Gelsolin (eg.  
CC familial amyloidosis of Finnish type), Fibrinogen (eg. hereditary renal  
CC amyloidosis), Lysozyme (eg. hereditary systemic amyloidosis). Other  
CC examples of amyloidogenic disorders include Huntington's disease and  
CC inclusion body myocytosis. The present sequence is human IgG1 heavy chain,  
CC used in the exemplification of the invention  
XX

SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 5; Length 232;  
Best Local Similarity 97.0%; Pred. No. 1.7e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EFKSCDKHTTCCPPCAPPELLGSPSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EFKSCDKHTTCCPPCAPPELLGSPSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NNYVDGVEVHNNKTKRREQYNSTRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEXT 120  
DB 61 NNYVDGVEVHNNKTKRREQYNSTRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEXT 120  
QY 121 ISKAVQPREPOVYTLPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTP 180  
DB 121 ISKAVQPREPOVYTLPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTP 180  
QY 121 ISKAGQPREPOVYTLPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTP 180  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMEALNHNHYOQRSLSPGK 232  
181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMEALNHNHYOQRSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMEALNHNHYOQRSLSPGK 232

RESULT 10  
ADJ57512  
ID ADJ57512 standard; protein; 232 AA.  
XX  
XX

AC ADJ57512;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
DE Herpes virus entry mediator-related protein #2.  
XX

KW therapeutic agent; endotoxin induced disease; fusion protein;  
KW Herpes virus entry mediator; HVEM; immunoglobulin Fc domain;  
KW endotoxic shock; human.  
XX  
XX  
XX Homo sapiens.  
XX  
XX JP2003128576-A.  
XX  
XX  
XX 08-MAY-2003.  
XX  
XX  
XX 25-OCT-2001; 2001JP-00328430.  
XX  
XX  
XX 25-OCT-2001; 2001JP-00328430.  
XX  
XX  
XX 25-OCT-2001; 2001JP-00328430.  
XX  
XX  
XX (TAIS) TAISHO PHARM CO LTD.  
XX (GENE-) GENE TECHNO SCI KK.  
XX  
XX  
XX MPI; 2003-817833/77.  
XX  
XX N-PSDB; ADJ57598.  
XX

PS Claim 5; SEQ ID NO 2; 11pp; Japanese.

CC The invention comprises a therapeutic agent for treating endotoxin  
CC induced disease, the therapeutic agent contains a fusion protein of the  
CC Herpes virus entry mediator (HVEM) protein and an immunoglobulin Fc  
CC domain. The therapeutic agent of the invention is useful for treating  
CC endotoxin induced disease, such as endotoxic shock. The present amino  
CC acid sequence represents a human protein which is claimed in the  
CC specification.  
XX

SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 7; Length 232;  
Best Local Similarity 97.0%; Pred. No. 1.7e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EFKSCDKHTTCCPPCAPPELLGSPSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EFKSCDKHTTCCPPCAPPELLGSPSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NNYVDGVEVHNNKTKRREQYNSTRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEXT 120  
DB 61 NNYVDGVEVHNNKTKRREQYNSTRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEXT 120  
QY 121 ISKAVQPREPOVYTLPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTP 180  
DB 121 ISKAVQPREPOVYTLPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTP 180  
QY 121 ISKAGQPREPOVYTLPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTP 180  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMEALNHNHYOQRSLSPGK 232  
181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMEALNHNHYOQRSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMEALNHNHYOQRSLSPGK 232

RESULT 11  
ADJ57512  
ID ADJ57512 standard; protein; 232 AA.  
XX  
XX  
XX ADJ57512;  
XX  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX  
XX Human IgG1 Fc domain fragment.  
XX  
XX

KW TF; tissue factor; FVIIa; factor VII; anticoagulant; thrombolytic;  
KW cerebroprotective; cytostatic; vasotropic; antithematic; antiarthritic;  
KW antiarteriosclerotic; antiinflammatory; antibacterial; immunosuppressive;  
KW hypertensive; cardiac; coagulation Factor VII; human; immunoglobulin G1;  
KW IgG1.  
XX

OS Homo sapiens.  
XX WO2004006962-A2.  
PN 22-JAN-2004.  
XX  
PD 09-JUL-2003; 2003WO-DK000481.  
XX  
PF 12-JUL-2002; 2002DK-00001099.  
XX  
PR (NOVO ) NOVO NORDISK AS.  
XX  
PA Bjorn SE, Nicolaisen EM, Steenstrup TD;  
XX WPI; 2004-180224/17.  
XX  
DR New compound binding to tissue factor, useful for treating diseases such  
XX as anglogenesis, ischemia/reperfusion, and rheumatoid arthritis.  
PT  
PS Claim 16; SEQ ID NO 7; 61pp; English.  
XX  
XX The invention relates to a compound (I) binding to tissue factor (TF).  
CC The compound (I) has the formula A-(LM)-C, where A is a PVIa  
CC polypeptide, LM is an optional linker group, C comprises an  
CC immunostimulatory effector domain, and (I) binds to TF. (I) inhibits TF-  
CC mediated activated factor VII (FVIIa) activity. (I) is useful as a  
CC medicament, and for the manufacture of a medicament for preventing or  
CC treating disease or disorder associated with pathophysiological TF  
CC activity. The disease or disorder associated with pathophysiological TF  
CC activity are deep venous thrombosis, arterial thrombosis, post surgical  
CC thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal  
CC coronary angioplasty (PTCA), stroke, cancer, tumor metastasis,  
CC arteriosclerosis and restenosis following angioplasty, acute and chronic  
CC indications such as inflammation, septic shock, septicemia, hypotension,  
CC adult respiratory distress syndrome (ARDS), disseminated intravascular  
CC coagulopathy (DIC), pulmonary embolism, platelet deposition, myocardial  
CC infarction, or prophylactic treatment of mammals with atherosclerotic  
CC vessels at risk for thrombosis. The present sequence represents the Fc  
CC domain fragment of human immunoglobulin G1 (IgG1).  
XX  
XX Sequence 232 AA;  
SQ  
Query Match 97.2%; Score 1225; DB 8; Length 232;  
Best Local Similarity 97.0%; Pred. No. 1.7e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPRSCDKHTHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPRSCDKHTHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMYVGVGHVHNKTKRREQYNSYTRVSVLVTLVHNNMNGEKYKKVSNKALPAIEKT 120  
DB 61 NMYVGVGHVHNKTKRREQYNSYTRVSVLVTLVHNNMNGEKYKKVSNKALPAIEKT 120  
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGOPENNYKTP 180  
DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGOPENNYKTP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYGQKSLSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYGQKSLSLSPGK 232  
RESULT 12  
ADRA48992  
ID ADRA48992 standard; peptide; 232 AA.  
XX  
XX ADRA48992;  
AC  
XX 02-DEC-2004 (first entry)  
DT Human IgG1 hinge and CH2 region.  
XX

XX anti-anemic; nephrotropic; human; HuEPO-L-vFc; erythropoietin; EPO;  
KW anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis;  
KW AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.  
XX  
OS Homo sapiens.  
XX US2004175824-A1.  
PN 09-SEP-2004.  
XX  
PD 21-JAN-2004; 2004US-00761593.  
XX  
PR 17-AUG-2001; 2001US-00932812.  
XX  
XX (SUNL/) SUN L K.  
PA (SUNB/) SUN B N C.  
PA (SUNC/) SUN C R Y.  
XX  
XX Sun LK, Sun BNC, Sun CRY;  
XX  
XX WPI; 2004-634851/61.  
XX  
XX New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin  
PT (HuEPO), a peptide linker, and a human IgG Fc variant, useful for  
PT treating chronic anemia due to renal diseases, cancer chemotherapy, or  
PT rheumatoid arthritis.  
XX  
PS Disclosure; SEQ ID NO 26; 31pp; English.  
XX  
XX A recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin  
CC (HuEPO), a peptide linker, and a human IgG Fc variant, is new.  
CC INDEPENDENT CLAIMS are also included for the following: a chinese hamster  
CC ovary (CHO)-derived cell line producing the HuEPO-L-vFc fusion protein in  
CC its growth medium in excess of 10 microg per million cells in a 24 hour  
CC period; and a method for making a recombinant fusion protein comprising  
CC HuEPO, a flexible peptide linker, and a human IgG Fc variant. Preferred  
CC protein: The peptide linker containing 20 or fewer amino acids is present  
CC between HuEPO and the human IgG Fc variant, and comprises two or more  
CC amino acids selected from glycine, serine, alanine, and threonine. The  
CC human IgG Fc variant comprises a hinge, CH2, and CH3 domains of human  
CC IgG2 with Pro31Ser mutation comprising 436 amino acids (SEQ ID NO. 18).  
CC It also comprises a hinge, CH2, and CH3 domains of human IgG4 with  
CC Ser228Pro and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO.  
CC 20). It further comprises a hinge, CH2, and CH3 domains of human IgB1  
CC with Leu234Val, Leu235Ala, and Pro333Ser mutations comprising 435 amino  
CC acids (SEQ ID NO. 22). The HuEPO-L-vFc fusion protein exhibits in vitro  
CC biological activity similar to or higher than that of rHuEPO on a molar  
CC basis. Preferred CHO-derived cell line: The CHO-derived cell line  
CC producing the HuEPO-L-vFc fusion protein in its growth medium in excess  
CC of 30 microg per million cells in a 24 hour period. The human IgG Fc  
CC variant comprises a hinge, CH2, CH3 domains of human IgG selected from  
CC IgB1 as SEQ ID NO. 22, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20,  
CC the IgG Fc contains amino acid mutations to attenuate effector functions,  
CC a flexible peptide linker containing 20 or fewer amino acids is present  
CC between HuEPO and human IgG Fc variant, and the HuEPO-L-vFc fusion  
CC protein exhibits in vitro biological activity similar to or higher than  
CC that of rHuEPO on a molar basis. Preferred method: Making a recombinant  
CC fusion protein comprising HuEPO, a flexible peptide linker, and a human  
CC IgG Fc variant comprises: generating a CHO-derived cell line; growing the  
CC cell line where the recombinant protein is expressed in its growth medium  
CC in excess of 10 microg per million cells in a 24 hour period; and  
CC purifying the expressed protein from (b), where the recombinant fusion  
CC protein exhibits in vitro biological activity similar to or higher than  
CC that of rHuEPO on a molar basis. Anti-anemic; Nephrotropic. No biological  
CC data given. None given. Administration can be through subcutaneous or  
CC intravenous route. No dosage given. The recombinant HuEPO-L-vFc fusion  
CC protein is useful for treating patients with chronic anemia due to renal  
CC diseases, cancer chemotherapy, rheumatoid arthritis, AZT treatment for  
CC HIV infection, or myelodysplastic syndrome. It is also useful in the  
CC treatment of renal failure. A fusion protein was assembled from several  
CC DNA segments. To obtain the gene encoding the leader peptide and mature  
CC protein of human erythropoietin (EPO), cDNA library of human fetal liver

or kidney was used as the template in polymerase chain reaction (PCR). For the convenience of cloning, SEQ ID NO. 1 which incorporates a restriction enzyme cleavage site is used as the 5' oligonucleotide primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon and incorporates a BamHI site. The resulting DNA fragments of approximately 600 bp were inserted into a holding vector such as pUC19 at the HindIII and BamHI sites to give the pEPO plasmid. The sequence of the human EPO gene was confirmed by DNA sequencing.

Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 8; Length 232;

Best Local Similarity 97.0%; Pred. No. 1.7e-88; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

OY 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
OY 61 NMVYDGVENVHNAKTKPREQVNSTYRVVSVLTTLHQMNGKEKCYKSNKALPAPIEKT 120
DB 61 NMVYDGVENVHNAKTKPREQVNSTYRVVSVLTTLHQMNGKEKCYKSNKALPAPIEKT 120
OY 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTT 180
DB 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTT 180
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DB 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTT 180
OY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALNHYOQRLSLSPGK 232
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALNHYOQRLSLSLSPGK 232

```

#### RESULT 13

AB09463 standard; protein; 233 AA.

AB09463;

01-JUL-2002 (first entry)

Human Igg Fc fragment amino acid sequence.

Protein A; immunoglobulin G; Igg; antibody; human.

Homo sapiens.

Key Location/Qualifiers

Misc-difference 168 /note= "encoded by GAC"

Misc-difference 169 /note= "encoded by ACC"

WO200204602-A1.

17-JAN-2002.

04-JUL-2001; 2001WO-JP005788.

07-JUL-2000; 2000JP-00206689.

(GENC-) GENCOM CORP.

Tanaka A, Ueda M, Teranishi Y,

WPI, 2002-148174/19.

N-PSDB; ABL52834.

Transformant yeast for stable supply of highly active catalytic antibody, comprises the capability of expressing and presenting protein A or its fragment, particularly with the 22 domain, on the cell surface.

Example 3; Fig 4; 25pp; Japanese.

The invention relates to a transformant yeast that can present protein A or its fragment on its cell surface. The yeast can be used for detecting or isolating the Fc part of immunoglobulin (Ig)G. The yeast is useful for a stable supply of highly active catalytic antibody e.g. by screening novel functional molecules and in isolating Fc-carrying secretory proteins. The yeast of the invention is capable of adhering specifically to a combinatorial antibody library with an Fc-carrying antibody component. The current sequence represents the human Igg Fc fragment amino acid sequence

Sequence 233 AA;

Query Match 97.2%; Score 1225; DB 5; Length 233;

Best Local Similarity 97.0%; Pred. No. 1.7e-88; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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OY 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 2 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 61
OY 61 NMVYDGVENVHNAKTKPREQVNSTYRVVSVLTTLHQMNGKEKCYKSNKALPAPIEKT 120
DB 62 NMVYDGVENVHNAKTKPREQVNSTYRVVSVLTTLHQMNGKEKCYKSNKALPAPIEKT 121
OY 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTT 180
DB 122 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTT 181
OY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALNHYOQRLSLSPGK 232
DB 182 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALNHYOQRLSLSLSPGK 233

```

#### RESULT 14

ABJ38647 standard; protein; 235 AA.

ABJ38647;

26-JUN-2003 (first entry)

pCXFc protein SEQ ID No 6.

Cytostatic; osteopathic; cerebroprotective; dermatological; enzyme; antigen binding; receptor protein tyrosine kinase; skeletal dysplasia;

constitutive activation; craniosynostosis; cell proliferative disorder; achondroplasia; thanatophoric dysplasia; acanthosis nigricans dysplasia;

hypochondroplasia; severe achondroplasia; transitional cell carcinoma; Muenke coronal craniosynostosis; Crouzin syndrome; acanthosis nigricans;

tumour progression; osteosarcoma; chondrosarcoma; multiple myeloma; mammary carcinoma; fibroblast growth factor receptor 3; FGFR3 protein.

Homo sapiens.

WO2002102854-A2.

27-DEC-2002.

20-JUN-2002; 2002WO-IB003523.

20-JUN-2001; 2001US-0299187P.

(MORP-) MORPHOSYS AG.

(PROC-) PROCHON BIOTECH LTD.

Thomassen-Wolf E, Borges E, Yayon A, Rom E;

WPI, 2003-167489/16.

N-PSDB; ABL40262.

New molecules having the antigen-binding portion of antibodies that block activation of receptor protein tyrosine kinase, useful for treating or inhibiting skeletal dysplasias, craniosynostosis or cell proliferative



PT disorders.

PS Example 2; Page 38; 103pp; English.

CC The invention relates to a novel molecule comprising the antigen binding  
CC portion of an isolated antibody, which has an increased affinity for a  
CC receptor protein tyrosine kinase and which blocks constitutive activation  
CC of the receptor protein tyrosine kinase. The methods and compositions of  
CC the invention are useful for treating or inhibiting a skeletal dysplasia,  
CC craniosynostosis or a cell proliferative disorder. The skeletal dysplasia  
CC is achondroplasia, rhizomelic dysplasia, hypochondroplasia, severe  
CC achondroplasia with developmental delay or acanthosis nigricans  
CC dysplasia. The craniosynostosis disorder is Menke coronal  
CC craniosynostosis or Crouzon syndrome with acanthosis nigricans. The cell  
CC proliferative disorder is tumour progression that is progression of  
CC transitional cell carcinoma, osteosarcoma, chondrosarcoma, multiple  
CC myeloma or mammary carcinoma. This sequence represents a protein derived  
CC from a pXfrc plasmid DNA vector relating to the protein tyrosine kinase  
CC inhibitor of the invention

**SQ** Sequence 235 AA;

Query Match	97.2%	Score 1225;	DB 6;	Length 235;
Best Local Similarity	97.0%	Pred. No. 1.7e-88;		
Matches 225; Conservative	3;	Mismatches 4;	Indels 0;	Gaps 0

QY	1	EPKSCDHTHTCCPCPAPBELLGGSPVFLPRPKYKOTLMSRPEYLCVVVVDVSHBDEPKXF	60
Db	4	EPKSCDHTHTCCPCPAPBELLGGSPVFLPRPKYKOTLMSRPEYLCVVVVDVSHBDEPKXF	63
QY	61	NMYVDGVEVHNHVKKRPBREQYNSTYRVVSVLTVLHQNMMNGKEKCYCKSNKALPAPIEKT	120
Db	64	NMYVDGVEVHNHVKKRPBREQYNSTYRVVSVLTVLHQNMMNGKEKCYCKSNKALPAPIEKT	123
QY	121	ISKAKVOPREBOVYTLPPSRDELTKNOVSLTCLVGFYPSDIAVEMESNGOPENNYKTPP	180
Db	124	ISKAKGPREBOVYTLPPSRDELTKNOVSLTCLVGFYPSDIAVEMESNGOPENNYKTPP	183
QY	181	PVLDVSQSFLLYSKULTVDKSRMOQGNVSCSYMEHALNNHVOQRSLSLSPGK 232	
Db	184	PVLDSDSFFLLYSKULTVDKSRMOQGNVSCSYMEHALNNHVOQRSLSLSPGK 235	

## RESULT 15

ID ADA89055 standard; protein; 235 AA.

AC ADA89055;

DT 20-NOV-2003 (first entry)

Plasmid pCXFc amino acid sequence SEQ ID NO:6.

XX antigen binding; antibody; specific binding affinity;  
KM receptor protein tyrosine kinase; RPTK;  
KM receptor protein tyrosine kinase inhibitor;  
KM fibroblast growth factor receptor; FGFR; osteopathic; cytostatic;  
KM ophthalmological; bone disorder; cartilage disorder; skeletal disorder;  
KM skeletal dysplasia; achondroplasia; thanatophoric dysplasia;  
KM hypochondroplasia; craniostenosis disorder;  
KM malignant cell proliferative disease; cancer; tumour; vision disorder;  
KM non-neoplastic angiogenic pathological condition.

OS Synthetic.

Homo sapiens.

PN WO2002102973-A2.

PD 27-DEC-2002

PF 20-JUN-2002; 2002WO-IL000495.

PR 20-JUN-2001; 2001US-0299187P

PA (PROC-) PROCHON BIOTECH LTD.

PI      yayon A,      Rom E;

DR WPI; 2003-175236/17.

DR N-PSDB; ADA89054.

PT New antibodies which have specific binding affinity for a receptor  
PT protein tyrosine kinase (RPTK) and block constitutive activation of  
PT useful for treating bone and cartilage disorders, or malignant cell  
PT proliferative diseases.

PS Example 2; Page 43; 122pp; English.

The present invention describes a molecule (1) comprising the antigen binding portion of an isolated antibody which has specific binding affinity for a receptor protein tyrosine kinase (RPTK), particularly for a fibroblast growth factor receptor (FGFR), and which blocks constitutive activation of an RPTK. Also described: (1) pharmaceutical compositions comprising (1) as an active ingredient and a pharmaceutical carrier, excipient, or auxiliary agent; (2) a kit comprising (1), at least one reagent for detecting the presence of (1) when bound to the RPTK, and instructions for use; (3) a method for treatment of bone and cartilage related disorders by administering a composition of (1) to the subject; (4) a method for treating or inhibiting a cell proliferative disease or disorder by administering the composition of (1); (5) a method for screening a molecule comprising the antigen-binding portion of an antibody which blocks ligand-dependent activation of RPTK; (6) an isolated nucleic acid molecule encoding a VL-CDR3 DNA region and a VH-CDR3 DNA region; (7) an isolated nucleic acid molecule encoding VL region and a VH region; (8) vectors comprising a nucleic acid molecule of (6) or (7); and (9) host cells transformed with the vector. (1) have osteopathic, cytostatic and ophthalmological activities, and can be used as a RPTK inhibitor. Compositions comprising (1) are useful for treating bone and cartilage disorders, including skeletal disorders such as skeletal dysplasia (achondroplasia, thanatophoric dysplasia, achondroplasia), severe achondroplasia with developmental delay and acanthosis nigricans dysplasia or a craniosynostosis disorder (e.g. Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis nigricans). The composition may also be used for treating or inhibiting malignant cell proliferative disease or disorder associated with abnormal RPTK activity, including a haematopoietic malignancy (e.g. multiple myeloma), solid tumours (e.g. mammary, colon, cervical, bladder, colorectal, chondrosarcoma or osteosarcoma), tumour formation, primary tumour, tumour progression (particularly progression of transitional cell carcinoma or mammary carcinoma), or tumour metastasis, where the cell proliferative disorder may be associated with the action of a constitutively activated RPTK, or with ligand-dependent activation of RPTK. The compositions may further be used for treating hyperproliferative diseases and disorders associated with ligand-dependent FGFR signaling, such as vision disorders (e.g. neovascular glaucoma, macular degeneration and proliferative retinopathy including diabetic retinopathy), and non-neoplastic angiogenic pathologic conditions (e.g. haemangiomas, angiodiomas and psoriasis). The present sequence is given in the exemplification of the present invention.

**SQ** Sequence 235 AA;

Query Match	97.2%	Score 1235	DB 6	Length 235
Best Local Similarity	97.0%	Pred. No. 1.7e+88		
Matches 225; Conservative	3	Mismatches 4	Indels 0	Gaps 0

Qy	1	EPKSDKHTHTOPCAPBELLGSPVFLPPKPKDITMTSRTEVTCVVVVDVSHDEBVKF	60
Db	4	EPKSDKHTHTOPCAPBELLGSPVFLPPKPKDITMTSRTEVTCVVVVDVSHDEBVKF	63
Qy	61	NMYVDGVEVHNKTKPREEQVNSTFRVSVLTVLHQNMNNGKXEYKCVSNKALPAIEKT	120
Db	64	NMYVDGVEVHNKTKPREEQVNSTFRVSVLTVLHQNMNNGKXEYKCVSNKALPAIEKT	123
Qy	121	ISKATVQPREPOVYTLPSRDELTKQVSLTCLVKGFIYSDIAVWESNGQPENNTKTTP	180

Db 124 ISKAGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTP 183  
QY 181 PVLDSVGSFFLYISKLTVDKSRWQGNVFSQSYMHEALHNHYOQRSISLSPGK 232  
Db 184 PVLDSVGSFFLYISKLTVDKSRWQGNVFSQSYMHEALHNHYOQRSISLSPGK 235

Search completed: June 7, 2005, 08:56:39  
Job time : 119.803 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: June 7, 2005, 09:01:44 ; Search time 101.775 Seconds

(without alignments)  
821.093 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260  
Sequence: 1 EPKSCDKHTHTCPCPAPPELL.....MHEALHNYQGRSLSPGK 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 1599520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications\_Aa:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1260	100.0	232	10 US-09-847-208-3	Sequence 3, Appl1
2	1260	100.0	232	14 US-10-000-439-3	Sequence 3, Appl1
3	1260	100.0	330	10 US-09-847-208-2	Sequence 2, Appl1
4	1260	100.0	330	14 US-10-000-439-2	Sequence 2, Appl1
5	1260	100.0	569	10 US-09-847-208-7	Sequence 7, Appl1
6	1260	100.0	569	14 US-10-000-439-7	Sequence 7, Appl1
7	1225	97.2	232	9 US-09-996-357-10	Sequence 10, Appl1
8	1225	97.2	232	10 US-09-389-782-1	Sequence 1, Appl1
9	1225	97.2	232	16 US-10-617-619-7	Sequence 7, Appl1
10	1225	97.2	232	16 US-10-761-593A-6	Sequence 26, Appl1
11	1225	97.2	232	16 US-10-831-622-97	Sequence 97, Appl1
12	1225	97.2	232	16 US-10-800-497-26	Sequence 26, Appl1

13	1225	97.2	232	16 US-10-800-449-26	Sequence 26, Appl1
14	1225	97.2	235	14 US-10-207-655-208	Sequence 208, App
15	1225	97.2	247	9 US-09-996-357-13	Sequence 13, Appl1
16	1225	97.2	251	14 US-10-008-063-18	Sequence 18, Appl1
17	1225	97.2	251	14 US-10-152-363A-6	Sequence 6, Appl1
18	1225	97.2	267	9 US-09-966-357-12	Sequence 12, Appl1
19	1225	97.2	288	10 US-09-822-851B-14	Sequence 14, Appl1
20	1225	97.2	288	14 US-10-119-637A-14	Sequence 14, Appl1
21	1225	97.2	329	15 US-10-370-749-48	Sequence 48, Appl1
22	1225	97.2	329	16 US-10-798-380-37	Sequence 37, Appl1
23	1225	97.2	330	10 US-09-995-898A-15	Sequence 15, Appl1
24	1225	97.2	330	10 US-09-892-949-38	Sequence 38, Appl1
25	1225	97.2	330	13 US-10-047-542-20	Sequence 20, Appl1
26	1225	97.2	330	14 US-10-269-805-68	Sequence 68, Appl1
27	1225	97.2	330	14 US-10-310-719-8	Sequence 8, Appl1
28	1225	97.2	330	14 US-10-112-582-1	Sequence 1, Appl1
29	1225	97.2	330	14 US-10-330-231A-81	Sequence 81, Appl1
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32	1225	97.2	330	15 US-10-420-034A-15	Sequence 15, Appl1
33	1225	97.2	330	15 US-10-257-907-5	Sequence 5, Appl1
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35	1225	97.2	330	16 US-10-679-620-58	Sequence 58, Appl1
36	1225	97.2	330	16 US-10-772-531-38	Sequence 38, Appl1
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38	1225	97.2	330	16 US-10-815-449-8	Sequence 8, Appl1
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41	1225	97.2	331	16 US-10-473-127-1863	Sequence 1663, Ap
42	1225	97.2	332	10 US-09-990-586-98	Sequence 98, Appl1
43	1225	97.2	332	14 US-10-310-113-167	Sequence 167, App
44	1225	97.2	332	14 US-10-230-880-98	Sequence 98, Appl1
45	1225	97.2	333	15 US-10-272-899A-8	Sequence 8, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-847-208-3  
; Sequence 3, Application US/09847208  
; Publication No. US20030082190A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; APPLICANT: Zhang, Ke  
; APPLICANT: Zhu, Daocheng  
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF  
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES  
; FILE REFERENCE: UC67.002A  
; CURRENT APPLICATION NUMBER: US/09/847,208  
; CURRENT FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 177  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-847-208-3

Query Match 100.0%; Score 1260; DB 10; Length 232;  
Best Local Similarity 100.0%; Pred. No. 9.8e-93;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 EFKSCDKHTHTCPCPAPPELLGSPSFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
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Db 121 ISKAVQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTT 180

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## RESULT 2

US-10-000-439-3

Sequence 3, Application US/10000439  
Publication No. US20030064063A1

GENERAL INFORMATION:

APPLICANT: Saxon, Andrew

TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
TREATMENT OF IMMUNE DISEASES

FILE REFERENCE: UC067.004A

CURRENT APPLICATION NUMBER: US/10/000,439

PRIOR FILING DATE: 2001-10-24

PRIOR APPLICATION NUMBER: US 09/847,208

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 232

TYPE: PRT

ORGANISM: Homo sapiens

US-10-000-439-3

Query Match 100.0%; Score 1260; DB 14; Length 232;  
Best Local Similarity 100.0%; Pred. No. 9.8e-93;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 181 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 232

Db 181 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 232

Qy 181 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 232

Db 181 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 232

Qy 181 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 232

Db 181 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 232

Qy 181 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 232

Db 181 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 232

Qy 181 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 232

Db 181 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 232

Qy 181 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 232

Db 181 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 232

Qy 181 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 232

Db 181 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 232

Qy 181 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 232

Db 181 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 232

Qy 1 EPKSCDKHTHTCPGPCAPPELLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60

Db 99 EPKSCDKHTHTCPGPCAPPELLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 158

Qy 61 NMVYDGEVHNVKTPREEQYNSTYRVVSVLTVLHQNMNNGKEYCKVSNKALPAPIEKT 120

Db 159 NMVYDGEVHNVKTPREEQYNSTYRVVSVLTVLHQNMNNGKEYCKVSNKALPAPIEKT 218

Qy 121 ISKAVQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTT 180

Db 219 ISKAVQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTT 278

Qy 181 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 232

Db 279 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 279 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Db 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

Qy 330 PVLDSVGSFPLYSKLTVDKSRWQOQNVFSCSVMEHALNHNHQQRSLSLSPGK 330

; NUMBER OF SEQ ID NOS: 177  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 569  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to CH2-CH3-CH4  
US-09-847-208-7

Query Match 100.0%; Score 1260; DB 10; Length 569;  
Best Local Similarity 100.0%; Pred. No. 2.8e-92;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKF 60  
Db 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKF 60  
Qy 61 NMYVDGVEVHNVKTKPREQYNSTYRVVSVLTVLHQNMNNGEKYCKVSNKALPAPIEKT 120  
Db 61 NMYVDGVEVHNVKTKPREQYNSTYRVVSVLTVLHQNMNNGEKYCKVSNKALPAPIEKT 120  
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKQVSLTCLVKGFTPSDIAVEMESNGQPENNYKTT 180  
Db 121 ISKAKVQPREPOVYTLPPSRDELTKQVSLTCLVKGFTPSDIAVEMESNGQPENNYKTT 180  
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVHHEALHNHYOQRSLSISPGK 232  
Db 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVHHEALHNHYOQRSLSISPGK 232

RESULT 6  
US-10-000-439-7  
; Sequence 7, Application US/10000439  
; Publication No. US20030064063A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES  
; FILE REFERENCE: UC067.004A  
; CURRENT APPLICATION NUMBER: US/10/000,439  
; CURRENT FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 09/847,208  
; PRIOR FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 569  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Fusion polypeptide comprising a hinge-CH2-CH3  
; OTHER INFORMATION: (IgG1) sequence and a CH2-CH3-CH4 (IgE) sequence  
US-10-000-439-7

Query Match 100.0%; Score 1260; DB 14; Length 569;  
Best Local Similarity 100.0%; Pred. No. 2.8e-92;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKF 60  
Db 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKF 60  
Qy 61 NMYVDGVEVHNVKTKPREQYNSTYRVVSVLTVLHQNMNNGEKYCKVSNKALPAPIEKT 120  
Db 61 NMYVDGVEVHNVKTKPREQYNSTYRVVSVLTVLHQNMNNGEKYCKVSNKALPAPIEKT 120  
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKQVSLTCLVKGFTPSDIAVEMESNGQPENNYKTT 180  
Db 121 ISKAKVQPREPOVYTLPPSRDELTKQVSLTCLVKGFTPSDIAVEMESNGQPENNYKTT 180  
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVHHEALHNHYOQRSLSISPGK 232

Db 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVHHEALHNHYOQRSLSISPGK 232

RESULT 7  
US-09-996-357-10  
; Sequence 10, Application US/09996357  
; Patent No. US20020133001A1  
; GENERAL INFORMATION:  
; APPLICANT: Gelfer, Malcolm L  
; APPLICANT: Isreal, David I  
; APPLICANT: Joyal, John L  
; APPLICANT: Gosselin, Michael  
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR  
; TITLE OF INVENTION: TREATING AN AMYLOIDOTIC DISEASE  
; FILE REFERENCE: PPI-105  
; CURRENT APPLICATION NUMBER: US/09/996,357  
; CURRENT FILING DATE: 2001-11-27  
; PRIOR APPLICATION NUMBER: 60/253,302  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/250,198  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/257,186  
; PRIOR FILING DATE: 2000-12-20  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-357-10

Query Match 97.2%; Score 1225; DB 9; Length 232;  
Best Local Similarity 97.0%; Pred. No. 6.1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKF 60  
Db 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKF 60  
Qy 61 NMYVDGVEVHNVKTKPREQYNSTYRVVSVLTVLHQNMNNGEKYCKVSNKALPAPIEKT 120  
Db 61 NMYVDGVEVHNVKTKPREQYNSTYRVVSVLTVLHQNMNNGEKYCKVSNKALPAPIEKT 120  
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKQVSLTCLVKGFTPSDIAVEMESNGQPENNYKTT 180  
Db 121 ISKAKVQPREPOVYTLPPSRDELTKQVSLTCLVKGFTPSDIAVEMESNGQPENNYKTT 180  
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVHHEALHNHYOQRSLSISPGK 232  
Db 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVHHEALHNHYOQRSLSISPGK 232

RESULT 8  
US-09-389-782-1  
; Sequence 1, Application US/09389782  
; Publication No. US20030144187A1  
; GENERAL INFORMATION:  
; APPLICANT: Wooden, Scott K.  
; APPLICANT: Mann, Michael B.  
; APPLICANT: Dunstan, Colin R.  
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods  
; FILE REFERENCE: A-604  
; CURRENT APPLICATION NUMBER: US/09/389,782  
; CURRENT FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Human  
US-09-389-782-1

Query Match 97.2%; Score 1225; DB 10; Length 232;  
Best Local Similarity 97.0%; Pred. No. 6, 1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTHTCPCPAPBLGSPVFLFPPPKDQTLMTSRTEVTCVVVDVSHEDPEVKF 60  
Db 1 EPKSCDKHTHTCPCPAPBLGSPVFLFPPPKDQTLMTSRTEVTCVVVDVSHEDPEVKF 60

Qy 61 NWYDVGVEVHNAKTKPREEOYNSTRVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120  
Db 61 NWYDVGVEVHNAKTKPREEOYNSTRVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120

Qy 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTTP 180  
Db 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTTP 180

Qy 181 PVLDSGSPFLYSKLTVDKSRWQOGNVFSCSVMEHALNHYTKSLSPGK 232  
Db 181 PVLDSGSPFLYSKLTVDKSRWQOGNVFSCSVMEHALNHYTKSLSPGK 232

## RESULT 9

US-10-617-619-7  
; Sequence 7, Application US/10617619  
; Publication No. US20040110929A1  
; GENERAL INFORMATION:  
; APPLICANT: Bjorn, Soren E  
; APPLICANT: Nicolaesen, Else M  
; APPLICANT: Jorgensen, Anker S  
; TITLE OF INVENTION: TF Binding Compound  
; FILE REFERENCE: 6455, 200-US  
; CURRENT APPLICATION NUMBER: US/10/617, 619  
; CURRENT FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01099  
; PRIOR FILING DATE: 2002-07-12  
; PRIOR APPLICATION NUMBER: US 60/404,568  
; PRIOR FILING DATE: 2002-08-19  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Human  
US-10-617-619-7

Query Match 97.2%; Score 1225; DB 16; Length 232;  
Best Local Similarity 97.0%; Pred. No. 6, 1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTHTCPCPAPBLGSPVFLFPPPKDQTLMTSRTEVTCVVVDVSHEDPEVKF 60  
Db 1 EPKSCDKHTHTCPCPAPBLGSPVFLFPPPKDQTLMTSRTEVTCVVVDVSHEDPEVKF 60

Qy 61 NWYDVGVEVHNAKTKPREEOYNSTRVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120  
Db 61 NWYDVGVEVHNAKTKPREEOYNSTRVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120

Qy 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTTP 180  
Db 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTTP 180

Qy 181 PVLDSGSPFLYSKLTVDKSRWQOGNVFSCSVMEHALNHYTKSLSPGK 232  
Db 181 PVLDSGSPFLYSKLTVDKSRWQOGNVFSCSVMEHALNHYTKSLSPGK 232

## RESULT 10

US-10-761-593A-26  
; Sequence 26, Application US/10761593A  
; Publication No. US20040175824A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Bill N

; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological  
; TITLE OF INVENTION: activities  
; FILE REFERENCE: 02SUN2001-A  
; CURRENT APPLICATION NUMBER: US/10/761,593A  
; CURRENT FILING DATE: 2004-01-21  
; PRIOR APPLICATION NUMBER: 09/932812  
; PRIOR FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 26  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-761-593A-26

Query Match 97.2%; Score 1225; DB 16; Length 232;  
Best Local Similarity 97.0%; Pred. No. 6, 1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTHTCPCPAPBLGSPVFLFPPPKDQTLMTSRTEVTCVVVDVSHEDPEVKF 60  
Db 1 EPKSCDKHTHTCPCPAPBLGSPVFLFPPPKDQTLMTSRTEVTCVVVDVSHEDPEVKF 60

Qy 61 NWYDVGVEVHNAKTKPREEOYNSTRVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120  
Db 61 NWYDVGVEVHNAKTKPREEOYNSTRVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120

Qy 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTTP 180  
Db 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTTP 180

Qy 181 PVLDSGSPFLYSKLTVDKSRWQOGNVFSCSVMEHALNHYTKSLSPGK 232  
Db 181 PVLDSGSPFLYSKLTVDKSRWQOGNVFSCSVMEHALNHYTKSLSPGK 232

## RESULT 11

US-10-831-622-97  
; Sequence 97, Application US/10831622  
; Publication No. US20040248257A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaye, Jonathan  
; APPLICANT: Wilkinson, Beverley  
; TITLE OF INVENTION: SPEX COMPOSITIONS AND METHODS OF USE  
; FILE REFERENCE: TSRI 810.1  
; CURRENT APPLICATION NUMBER: US/10/831,622  
; CURRENT FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US 60/467,206  
; PRIOR FILING DATE: 2003-04-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 97  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-831-622-97

Query Match 97.2%; Score 1225; DB 16; Length 232;  
Best Local Similarity 97.0%; Pred. No. 6, 1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTHTCPCPAPBLGSPVFLFPPPKDQTLMTSRTEVTCVVVDVSHEDPEVKF 60  
Db 1 EPKSCDKHTHTCPCPAPBLGSPVFLFPPPKDQTLMTSRTEVTCVVVDVSHEDPEVKF 60

Qy 61 NWYDVGVEVHNAKTKPREEOYNSTRVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120  
Db 61 NWYDVGVEVHNAKTKPREEOYNSTRVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120

Qy 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTTP 180  
Db 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTTP 180

QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALNHNHYQORSLSPGK 232  
Best Local Similarity 97.0%; Score 1225; DB 16; Length 232;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

## RESULT 12

US-10-800-497-26  
; Sequence 26, Application US/10800497  
; Publication No. US20040259209A1  
; GENERAL INFORMATION:

APPLICANT: Sun, Lee-Hwei K  
APPLICANT: Sun, Bill  
TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-  
stimulating factor with  
TITLE OF INVENTION: increased biological activities  
FILE REFERENCE: 03SUN2001  
CURRENT APPLICATION NUMBER: US/10/800,497  
CURRENT FILING DATE: 2004-03-15  
PRIOR APPLICATION NUMBER: US/09/968,362  
PRIOR FILING DATE: 2001-10-01  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 26  
LENGTH: 232  
TYPE: PRT

ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains  
US-10-800-497-26

Query Match 97.2%; Score 1225; DB 16; Length 232;  
Best Local Similarity 97.0%; Pred. No. 6.1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
1 EPKSCDKHTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 61 NMYVDGVEVHNAKTPRREQYNSTRVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 120  
61 NMYVDGVEVHNAKTPRREQYNSTRVSVLTVLHODMNGKEYCKVSNKALPAPIEKT 120  
DB 121 ISKAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKTT 180  
121 ISKAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKTT 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALNHNHYQORSLSPGK 232  
181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALNHNHYQORSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALNHNHYQORSLSPGK 232

## RESULT 13

US-10-800-449-26  
; Sequence 26, Application US/10800449  
; Publication No. US20040265973A1  
; GENERAL INFORMATION:

APPLICANT: Sun, Lee-Hwei K  
APPLICANT: Sun, Bill  
TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor  
TITLE OF INVENTION: increased biological activities  
FILE REFERENCE: 03SUN2001  
CURRENT APPLICATION NUMBER: US/10/800,449  
CURRENT FILING DATE: 2004-03-15  
PRIOR APPLICATION NUMBER: US/09/968,362  
PRIOR FILING DATE: 2001-10-01  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 26  
LENGTH: 232  
TYPE: PRT

ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains  
US-10-800-449-26

Query Match 97.2%; Score 1225; DB 16; Length 232;  
Best Local Similarity 97.0%; Pred. No. 6.1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
1 EPKSCDKHTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 61 NMYVDGVEVHNAKTPRREQYNSTRVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 120  
61 NMYVDGVEVHNAKTPRREQYNSTRVSVLTVLHODMNGKEYCKVSNKALPAPIEKT 120  
DB 121 ISKAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKTT 180  
121 ISKAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKTT 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALNHNHYQORSLSPGK 232  
181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALNHNHYQORSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALNHNHYQORSLSPGK 232

## RESULT 14

US-10-207-655-208  
; Sequence 208, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:

APPLICANT: Ledbetter, Jeffrey A.  
APPLICANT: Hayden-Ledbetter, Martha S.  
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
FILE REFERENCE: 390069, 401C1  
CURRENT APPLICATION NUMBER: US/10/207,655  
CURRENT FILING DATE: 2002-07-25  
NUMBER OF SEQ ID NOS: 426  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 208  
LENGTH: 235  
TYPE: PRT

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Fusion polypeptide  
US-10-207-655-208

Query Match 97.2%; Score 1225; DB 14; Length 235;  
Best Local Similarity 97.0%; Pred. No. 6.2e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
1 EPKSCDKHTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 4 EPKSCDKHTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 63  
61 NMYVDGVEVHNAKTPRREQYNSTRVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 120  
61 NMYVDGVEVHNAKTPRREQYNSTRVSVLTVLHODMNGKEYCKVSNKALPAPIEKT 123  
DB 121 ISKAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKTT 180  
121 ISKAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKTT 183  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALNHNHYQORSLSPGK 232  
181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALNHNHYQORSLSPGK 235  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALNHNHYQORSLSPGK 235

## RESULT 15

US-09-996-357-13  
; Sequence 13, Application US/09996357  
; Patent No. US20020133001A1  
; GENERAL INFORMATION:

APPLICANT: Gefter, Malcolm L  
APPLICANT: Israel, David I  
APPLICANT: Joyal, John L  
APPLICANT: Gosselin, Michael



;; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR  
;; TITLE OF INVENTION: TREATING AN AMYLOIDOGENIC DISEASE  
;; FILE REFERENCE: PPI-105  
;; CURRENT APPLICATION NUMBER: US/09/996,357  
;; CURRENT FILING DATE: 2001-11-27  
;; PRIOR APPLICATION NUMBER: 60/253,302  
;; PRIOR FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: 60/250,198  
;; PRIOR FILING DATE: 2000-11-29  
;; PRIOR APPLICATION NUMBER: 60/257,186  
;; PRIOR FILING DATE: 2000-12-20  
;; NUMBER OF SEQ ID NOS: 13  
;; SOFTWARE: Patentin Ver. 2.0  
;; SEQ ID NO 13  
;; LENGTH: 247  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-996-357-13

Query Match 97.2%; Score 1225; DB 9; Length 247;  
Best Local Similarity 97.0%; Pred. No. 6,6e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 16 EPKSCDKHTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 75  
QY 61 NWYVDGVEVHNKTRPREQVNSTYRVVSVLTVTHQNMNGKEKCKVSNKALPAPIEKT 120  
DB 76 NWYVDGVEVHNKTRPREQVNSTYRVVSVLTVTHQNMNGKEKCKVSNKALPAPIEKT 135  
QY 121 ISKATVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNNGQPENNYKTT 180  
DB 136 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNNGQPENNYKTT 195  
QY 181 PVLDSVGSFFLYSKLTIVKSRWQQGNVFCSMHEALHNRHYOORSLSLSPGK 232  
DB 196 PVLDSVGSFFLYSKLTIVKSRWQQGNVFCSMHEALHNRHYOORSLSLSPGK 247

Search completed: June 7, 2005, 09:25:07  
Job time : 102.775 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 08:49:07 ; Search time 32.456 Seconds  
(without alignments)  
533.603 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260

Sequence: 1 EPKSCDKHTHTCPCPAPPELL.....MHEALHNHYQQRSLSPGK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*

2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*

3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*

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5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*

6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	97.2	232	2 US-08-595-043A-50	Sequence 50, Appl
2	1225	97.2	232	4 US-09-968-362A-26	Sequence 26, Appl
3	1225	97.2	331	4 US-09-178-869-2	Sequence 2, Appl
4	1225	97.2	331	4 US-09-761-413-2	Sequence 2, Appl
5	1225	97.2	360	3 US-09-180-100-11	Sequence 11, Appl
6	1225	97.2	371	1 US-08-236-311-7	Sequence 7, Appl
7	1225	97.2	371	4 US-08-457-918-7	Sequence 7, Appl
8	1225	97.2	371	4 US-10-157-408-7	Sequence 7, Appl
9	1225	97.2	376	3 US-09-180-100-22	Sequence 22, Appl
10	1225	97.2	396	2 US-08-784-512-3	Sequence 3, Appl
11	1225	97.2	424	5 US-09-176-228-3	Sequence 12, Appl
12	1225	97.2	424	5 PCT-US95-03866-12	Sequence 14, Appl
13	1225	97.2	424	5 PCT-US85-03866-14	Sequence 11, Appl
14	1225	97.2	437	5 PCT-US96-10043-11	Sequence 9, Appl
15	1225	97.2	442	4 US-08-472-888A-7	Sequence 7, Appl
16	1225	97.2	446	5 PCT-US96-10043-9	Sequence 7, Appl
17	1225	97.2	449	1 US-08-397-411-7	Sequence 13, Appl
18	1225	97.2	452	4 US-08-458-516-13	Sequence 16, Appl
19	1225	97.2	459	1 US-09-773-877B-16	Sequence 18, Appl
20	1225	97.2	462	4 US-09-773-877B-18	Sequence 41, Appl
21	1225	97.2	467	4 US-08-030-175-41	Sequence 42, Appl
22	1225	97.2	475	4 US-09-740-002-27	Sequence 10, Appl
23	1225	97.2	476	2 US-08-378-939-10	Sequence 4, Appl
24	1225	97.2	476	3 US-08-487-550-4	Sequence 12, Appl
25	1225	97.2	476	3 US-08-487-550-4	Sequence 12, Appl
26	1225	97.2	476	3 US-08-487-550-4	Sequence 12, Appl
27	1225	97.2	476	3 US-08-487-550-4	Sequence 12, Appl

28	1225	97.2	476	4 US-09-526-098-4	Sequence 4, Appl
29	1225	97.2	476	4 US-09-526-098-12	Sequence 12, Appl
30	1225	97.2	476	4 US-09-383-916-4	Sequence 4, Appl
31	1225	97.2	476	4 US-09-383-916-12	Sequence 12, Appl
32	1225	97.2	478	3 US-08-487-550-8	Sequence 8, Appl
33	1225	97.2	478	4 US-09-526-098-8	Sequence 8, Appl
34	1225	97.2	478	4 US-09-383-916-8	Sequence 8, Appl
35	1225	97.2	497	4 US-09-499-846-6	Sequence 6, Appl
36	1225	97.2	525	4 US-09-499-846-4	Sequence 4, Appl
37	1225	97.2	525	4 US-09-746-359A-54	Sequence 54, Appl
38	1225	97.2	557	4 US-09-773-877B-14	Sequence 14, Appl
39	1225	97.2	567	4 US-09-825-561A-16	Sequence 16, Appl
40	1225	97.2	567	4 US-09-773-877B-12	Sequence 12, Appl
41	1225	97.2	567	4 US-09-773-877B-20	Sequence 20, Appl
42	1225	97.2	571	4 US-09-746-359A-53	Sequence 53, Appl
43	1225	97.2	592	4 US-09-313-942-8	Sequence 8, Appl
44	1225	97.2	622	4 US-09-499-846-2	Sequence 2, Appl
45	1225	97.2	859	4 US-09-313-942-7	Sequence 7, Appl

ALIGNMENTS

```
RESULT 1
US-08-595-043A-50
; Sequence 50, Application US/08595043A
; Patent No. 5935824
;
; GENERAL INFORMATION:
; APPLICANT: SCARLATO, GREGORY D.
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,043A
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32, 837
; REFERENCE/DOCKET NUMBER: SGAR-00371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-595-043A-50

Query Match      97.2%  Score 1225;  DB 2;  Length 232;
Best Local Similarity 97.0%  Pred. No. 3 6e-116;
Matches 225;  Conservative 3;  Mismatches 4;  Indels 0;  Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLFPKPKDITMISRTPEVTCVVVDVSHEDPEVKF 60
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DB 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLFPKPKDITMISRTPEVTCVVVDVSHEDPEVKF 60
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QY 61 NMYVDGVEVHANKTPREKQYNSTYRVSVLTVTHQNMNNGEYKKKSKNKAIPAIETKT 120
   |||
DB 61 NMYVDGVEVHANKTPREKQYNSTYRVSVLTVTHQNMNNGEYKKKSKNKAIPAIETKT 120
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Qy 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 180
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Db 121 ISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 180

Qy 181 PVLDSVGSFPLYSKLTVDKSRWQGNVSCSVMEHALNHNHYQKSLSPGK 232
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Db 181 PVLDSGSFPLYSKLTVDKSRWQGNVSCSVMEHALNHNHYQKSLSPGK 232

RESULT 2
US-09-968-362A-26
; Sequence 26, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: FC fusion proteins of human granulocyte colony-stimulating factor
; TITLE OF INVENTION: Increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362A
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human Igg1 Fc with native hinge, CH2 and CH3 domains
US-09-968-362A-26

Query Match 97.2%; Score 1225; DB 4; Length 232;
Best Local Similarity 97.0%; Pred. No. 3,6e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTHTCPPCAPPELLGSPVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKF 60
|||
Db 1 EPKSCDKHTHTCPPCAPPELLGSPVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKF 60

Qy 61 NWYDGVGVHNAKTPREEQNSTYRVVSVLTVLIHQNMNGEKYCKVSNKALPAPIEKT 120
|||
Db 61 NWYDGVGVHNAKTPREEQNSTYRVVSVLTVLIHQNMNGEKYCKVSNKALPAPIEKT 120

Qy 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 180
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Db 121 ISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 180

Qy 181 PVLDSVGSFPLYSKLTVDKSRWQGNVSCSVMEHALNHNHYQKSLSPGK 232
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Db 181 PVLDSGSFPLYSKLTVDKSRWQGNVSCSVMEHALNHNHYQKSLSPGK 232

RESULT 3
US-09-178-869-2
; Sequence 2, Application US/09178869B
; Patent No. 6197234
; GENERAL INFORMATION:
; APPLICANT: Tao, Weng
; APPLICANT: Wong, Shou
; APPLICANT: Hickey, William F
; APPLICANT: Hamman, Joseph P.
; APPLICANT: Baetge, E. Edward
; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
; FILE REFERENCE: 17810-043
; CURRENT APPLICATION NUMBER: US/09/178,869B
; CURRENT FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-869-2
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Query Match 97.2%; Score 1225; DB 3; Length 331;
Best Local Similarity 97.0%; Pred. No. 6,1e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTHTCPPCAPPELLGSPVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKF 60
|||
Db 100 EPKSCDKHTHTCPPCAPPELLGSPVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKF 159

Qy 61 NWYDGVGVHNAKTPREEQNSTYRVVSVLTVLIHQNMNGEKYCKVSNKALPAPIEKT 120
|||
Db 160 NWYDGVGVHNAKTPREEQNSTYRVVSVLTVLIHQNMNGEKYCKVSNKALPAPIEKT 219

Qy 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 180
|||
Db 220 ISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 279

Qy 181 PVLDSVGSFPLYSKLTVDKSRWQGNVSCSVMEHALNHNHYQKSLSPGK 232
|||
Db 280 PVLDSGSFPLYSKLTVDKSRWQGNVSCSVMEHALNHNHYQKSLSPGK 331

RESULT 4
US-09-761-413-2
; Sequence 2, Application US/09761413
; Patent No. 6506891
; GENERAL INFORMATION:
; APPLICANT: Tao, Weng
; APPLICANT: Wong, Shou
; APPLICANT: Hickey, William F
; APPLICANT: Hamman, Joseph P.
; APPLICANT: Baetge, E. Edward
; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
; FILE REFERENCE: 17810-043
; CURRENT APPLICATION NUMBER: US/09/761,413
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US/09/178,869
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-413-2

Query Match 97.2%; Score 1225; DB 4; Length 331;
Best Local Similarity 97.0%; Pred. No. 6,1e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTHTCPPCAPPELLGSPVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKF 60
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Qy 61 NWYDGVGVHNAKTPREEQNSTYRVVSVLTVLIHQNMNGEKYCKVSNKALPAPIEKT 120
|||
Db 160 NWYDGVGVHNAKTPREEQNSTYRVVSVLTVLIHQNMNGEKYCKVSNKALPAPIEKT 219

Qy 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 180
|||
Db 220 ISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 279

Qy 181 PVLDSVGSFPLYSKLTVDKSRWQGNVSCSVMEHALNHNHYQKSLSPGK 232
|||
Db 280 PVLDSGSFPLYSKLTVDKSRWQGNVSCSVMEHALNHNHYQKSLSPGK 331

RESULT 5
US-09-180-100-11
; Sequence 11, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 630639510
```

APPLICANT: NAGATA, Shigekazu  
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE  
FILE REFERENCE: 1110-207P  
CURRENT APPLICATION NUMBER: US/09/180,100  
CURRENT FILING DATE: 1998-11-02  
EARLIER APPLICATION NUMBER: PCT/JP97/01502  
EARLIER FILING DATE: 1997-05-01  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 11  
LENGTH: 360  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-180-100-11

Query Match 97.2% Score 1225; DB 3; Length 360;  
Best Local Similarity 97.0%; Pred. No. 6,9e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 BEKSCDKHTHCPCPAPBLGGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 129 BEKSCDKHTHCPCPAPBLGGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 188  
DB 189 NMVYDGEVHNAKTRPEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 248  
QY 121 ISKAVQPREPOVYTLPSRDELTKNOVSLTCLVNGFYPSDIAVENESGOPENNYKTP 180  
DB 249 ISKAGQPREPOVYTLPSRDELTKNOVSLTCLVNGFYPSDIAVENESGOPENNYKTP 308  
QY 181 PVLDSGSEFLYSKLTVDKSRWQGNVSCSYMHKALHNHYOQRSLSIPGK 232  
DB 309 PVLDSGSEFLYSKLTVDKSRWQGNVSCSYMHKALHNHYOQRSLSIPGK 360

## RESULT 6

US-08-236-311-7  
Sequence 7, Application US/08236311  
Patent No. 5565335  
GENERAL INFORMATION:  
APPLICANT: Capon, Daniel J.  
APPLICANT: Gregory, Timothy J.  
TITLE OF INVENTION: Adheson Variants  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/236,311  
FILING DATE: 02-MAY-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/936190  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/842777  
FILING DATE: 18-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/250785  
FILING DATE: 28-SEP-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/104329  
FILING DATE: 02-OCT-1987

ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 444PIC2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 371 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-236-311-7

Query Match 97.2% Score 1225; DB 1; Length 371;  
Best Local Similarity 97.0%; Pred. No. 7,2e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 BEKSCDKHTHCPCPAPBLGGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 140 BEKSCDKHTHCPCPAPBLGGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 199  
DB 200 NMVYDGEVHNAKTRPEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 259  
QY 121 ISKAVQPREPOVYTLPSRDELTKNOVSLTCLVNGFYPSDIAVENESGOPENNYKTP 180  
DB 260 ISKAGQPREPOVYTLPSRDELTKNOVSLTCLVNGFYPSDIAVENESGOPENNYKTP 319  
QY 181 PVLDSGSEFLYSKLTVDKSRWQGNVSCSYMHKALHNHYOQRSLSIPGK 232  
DB 320 PVLDSGSEFLYSKLTVDKSRWQGNVSCSYMHKALHNHYOQRSLSIPGK 371

## RESULT 7

US-08-457-918-7  
Sequence 7, Application US/08457918  
Patent No. 6117655  
GENERAL INFORMATION:  
APPLICANT: Capon, Daniel J.  
APPLICANT: Gregory, Timothy J.  
TITLE OF INVENTION: Adheson Variants  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/457,918  
FILING DATE: 1-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/236311  
FILING DATE: 02-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/936190  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/842777  
FILING DATE: 18-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/250785  
FILING DATE: 28-SEP-1988

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/104329  
FILING DATE: 02-OCT-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubinec, Jeffrey S.  
REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0444P1C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8228  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 371 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-457-918-7

Query Match 97.2%; Score 1225; DB 3; Length 371;  
Best Local Similarity 97.0%; Pred. No. 7.2e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EFKSCDKHTHTCPCPAPBLGGPSVFLPPPKKDTLMTSRTPVTCVVVDVSHEDPEVKF 60  
DB 140 EFKSCDKHTHTCPCPAPBLGGPSVFLPPPKKDTLMTSRTPVTCVVVDVSHEDPEVKF 199  
QY 61 NMYVDGVEVHNAKTRPEEQYNSTYRVVSVLTVLIHQNMNGKEYCKVSNKALPAPIEKT 120  
DB 200 NMYVDGVEVHNAKTRPEEQYNSTYRVVSVLTVLIHQDMINGKEYCKVSNKALPAPIEKT 259  
QY 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
DB 260 ISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 319  
QY 181 PVLDSGSEFLYKSLTVDSKRWQGNVFCSCYMHGALHNHYQOBSLSLSPGK 232  
DB 320 PVLDSGSEFLYKSLTVDSKRWQGNVFCSCYMHGALHNHYQOBSLSLSPGK 371

RESULT 8  
US-10-157-408-7  
Sequence 7, Application US/10157408  
Patent No. 6710169  
GENERAL INFORMATION:  
APPLICANT: Capon, Daniel J.  
Gregory, Timothy J.  
TITLE OF INVENTION: Adhesion Variants  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/157,408  
FILING DATE: 28-May-2002  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/457,918  
FILING DATE: 1-JUN-1995  
APPLICATION NUMBER: 08/236311  
FILING DATE: 02-MAY-1994  
APPLICATION NUMBER: 07/936190  
FILING DATE: 26-AUG-1992  
APPLICATION NUMBER: 07/842777  
FILING DATE: 18-FEB-1992

APPLICATION NUMBER: 07/250785  
FILING DATE: 28-SEP-1988  
APPLICATION NUMBER: 07/104329  
FILING DATE: 02-OCT-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubinec, Jeffrey S.  
REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0444P1C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8228  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 371 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-157-408-7

Query Match 97.2%; Score 1225; DB 4; Length 371;  
Best Local Similarity 97.0%; Pred. No. 7.2e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EFKSCDKHTHTCPCPAPBLGGPSVFLPPPKKDTLMTSRTPVTCVVVDVSHEDPEVKF 60  
DB 140 EFKSCDKHTHTCPCPAPBLGGPSVFLPPPKKDTLMTSRTPVTCVVVDVSHEDPEVKF 199  
QY 61 NMYVDGVEVHNAKTRPEEQYNSTYRVVSVLTVLIHQNMNGKEYCKVSNKALPAPIEKT 120  
DB 200 NMYVDGVEVHNAKTRPEEQYNSTYRVVSVLTVLIHQDMINGKEYCKVSNKALPAPIEKT 259  
QY 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
DB 260 ISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 319  
QY 181 PVLDSGSEFLYKSLTVDSKRWQGNVFCSCYMHGALHNHYQOBSLSLSPGK 232  
DB 320 PVLDSGSEFLYKSLTVDSKRWQGNVFCSCYMHGALHNHYQOBSLSLSPGK 371

RESULT 9  
US-09-180-100-22  
Sequence 22, Application US/09180100  
Patent No. 6306395  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, No. 630639510  
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE  
FILE REFERENCE: 1110-207P  
CURRENT APPLICATION NUMBER: US/09/180,100  
CURRENT FILING DATE: 1998-11-02  
EARLIER APPLICATION NUMBER: PCT/JP97/01502  
EARLIER FILING DATE: 1997-05-01  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 22  
LENGTH: 376  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-180-100-22

Query Match 97.2%; Score 1225; DB 3; Length 376;  
Best Local Similarity 97.0%; Pred. No. 7.3e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EFKSCDKHTHTCPCPAPBLGGPSVFLPPPKKDTLMTSRTPVTCVVVDVSHEDPEVKF 60  
DB 145 EFKSCDKHTHTCPCPAPBLGGPSVFLPPPKKDTLMTSRTPVTCVVVDVSHEDPEVKF 204  
QY 61 NMYVDGVEVHNAKTRPEEQYNSTYRVVSVLTVLIHQNMNGKEYCKVSNKALPAPIEKT 120  
DB 205 NMYVDGVEVHNAKTRPEEQYNSTYRVVSVLTVLIHQDMINGKEYCKVSNKALPAPIEKT 264

QY 121 ISKAVQPREPOVYTLPPSRDELTKQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTP 180  
DB 265 ISKAGOPREPOVYTLPPSRDELTKQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTP 324  
QY 181 PVLDSGSPFLYSKLTVDKSRWQGNVFSQVMEALHNHYOQRSLSPGK 232  
DB 345 PVLDSGSPFLYSKLTVDKSRWQGNVFSQVMEALHNHYOQRSLSPGK 376

## RESULT 10

US-08-784-512-3  
; Sequence 3, Application US/08784512  
; Patent No. 5872209  
; GENERAL INFORMATION:  
; APPLICANT: BARTNIK, Eckart  
; APPLICANT: EIDENMUELLER, Bernd  
; APPLICANT: BUETTNER, Frank  
; APPLICANT: CATERSON, Bruce  
; APPLICANT: HUGHES, Clare  
; TITLE OF INVENTION: An artificial recombinant substrate (RAGG 1)  
; TITLE OF INVENTION: and native aggregan to study the proteolytic activity of  
; TITLE OF INVENTION: "Aggreganase" in cell culture systems  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/784,512  
; FILING DATE: 17-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 96100682.2  
; FILING DATE: 18-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRANADOS, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 18748/311  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 396 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..396  
; US-08-784-512-3

Query Match 97.2%; Score 1225; DB 2; Length 396;

Best Local Similarity 97.0%; Pred. No. 7, 9e-116; Indels 0; Gaps 0;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPELLGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 165 EPKSCDKHTHTCPCPAPELLGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKF 224  
QY 61 NMYVDGVEVHNAKTKRREQDYNSTYRVVSVLTVLHQDNMNGEKYKCKVSNKALPAPIEKT 120  
DB 225 NMYVDGVEVHNAKTKRREQDYNSTYRVVSVLTVLHQDNMNGEKYKCKVSNKALPAPIEKT 284

QY 121 ISKAVQPREPOVYTLPPSRDELTKQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTP 180  
DB 265 ISKAGOPREPOVYTLPPSRDELTKQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTP 344  
QY 181 PVLDSGSPFLYSKLTVDKSRWQGNVFSQVMEALHNHYOQRSLSPGK 232  
DB 345 PVLDSGSPFLYSKLTVDKSRWQGNVFSQVMEALHNHYOQRSLSPGK 336

## RESULT 11

US-09-176-228-3  
; Sequence 3, Application US/09176228  
; Patent No. 6180334  
; GENERAL INFORMATION:  
; APPLICANT: BARTNIK, Eckart  
; APPLICANT: EIDENMUELLER, Bernd  
; APPLICANT: BUETTNER, Frank  
; APPLICANT: CATERSON, Bruce  
; APPLICANT: HUGHES, Clare  
; TITLE OF INVENTION: An artificial recombinant substrate (RAGG 1)  
; TITLE OF INVENTION: and native aggregan to study the proteolytic activity of  
; TITLE OF INVENTION: "Aggreganase" in cell culture systems  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/176,228  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/784,512  
; FILING DATE: 17-JAN-1997  
; APPLICATION NUMBER: EP 96100682.2  
; FILING DATE: 18-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRANADOS, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 18748/311  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 396 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..396  
; US-09-176-228-3

Query Match 97.2%; Score 1225; DB 3; Length 396;

Best Local Similarity 97.0%; Pred. No. 7, 9e-116; Indels 0; Gaps 0;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPELLGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 165 EPKSCDKHTHTCPCPAPELLGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKF 224  
QY 61 NMYVDGVEVHNAKTKRREQDYNSTYRVVSVLTVLHQDNMNGEKYKCKVSNKALPAPIEKT 120  
DB 225 NMYVDGVEVHNAKTKRREQDYNSTYRVVSVLTVLHQDNMNGEKYKCKVSNKALPAPIEKT 284

QY	12	285	181	345
ISAKYQPRPQVYTLPSRDELTKNOVSLTGLYGFPSDLAIAWMSNGPENNYTTP	ISAKYQPRPQVYTLPSRDELTKNOVSLTGLYGFPSDLAIAWMSNGPENNYTTP	PVLDVSGFPLYSKLTVDKSRMOQGVSCSYMEALNNHYQKSLSLSPK	PVLDSDGSFPLYSKLTVDKSRMOQGVSCSYMEALNNHYQKSLSLSPK	
Db	285	181	345	
ISAKYQPRPQVYTLPSRDELTKNOVSLTGLYGFPSDLAIAWMSNGPENNYTTP	PVLDVSGFPLYSKLTVDKSRMOQGVSCSYMEALNNHYQKSLSLSPK	PVLDSDGSFPLYSKLTVDKSRMOQGVSCSYMEALNNHYQKSLSLSPK		

RESULT 12  
PCT-US95-03866-12  
; Sequence 12, Application PC/TUS9503866

APPLICANT: Cytomed, Inc. (all states except US)  
 APPLICANT: Nocke, Karl (US only)  
 APPLICANT: Lobell, Robert B (US only)  
 TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND  
 TITLE OF INVENTION: FLT-3/FLK-2 LIGAND  
 NUMBER OF SEQUENCES: 36  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Neave  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10020  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/03866  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/220,379  
 FILING DATE: 28-MAR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Haley Jr, James F  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: Cytomed/2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-596-9000  
 TELEFAX: 212-596-9090  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 424 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US95-03866-12

Query Match	97.2%	Score 1235	DB 5	Length 424
Best Local	97.0%	Pred. No. 8.7e-116		
Matches 225	Conservative	3	Mismatches 4	Indels 0
				Gaps 0

QY	1	EPKSCOKTHCPCPAPAPELLGGSPVFLPPKCKDTLMTSRPBPVYCVVVDVSHSDPEVKF	60
	193	EPKSCOKTHCPCPAPAPELLGGSPVFLPPKCKDTLMTSRPBPVYCVVVDVSHSDPEVKF	252
QY	61	NMYVDGEVHNVTCKRREQYNSTYRVSVLTVLTHQNNMGKCYKCKVSNKALPAPIEKT	120
	253	NMYVDGEVHNVTCKRREQYNSTYRVSVLTVLTHQNNMGKCYKCKVSNKALPAPIEKT	312
QY	121	ISKAKVQPREPQVYTLPSRDELTKNQVSLTCLVKGFPSPDIAVEMESNGPENNYYKTP	180
	313	ISKAKVQPREPQVYTLPSRDELTKNQVSLTCLVKGFPSPDIAVEMESNGPENNYYKTP	372
QY	181	PVLDISGSPFLYSKLTVDKSRKQOGVWFCSTVMEALNNHTQKSLSLSPK	232
	373	PVLDISGSPFLYSKLTVDKSRKQOGVWFCSTVMEALNNHTQKSLSLSPK	424

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1      RESULT 13
2      PCT-US95-03866-14
3      : Sequence 14, Application PC/TUS9503866
4      : GENERAL INFORMATION:
5      : APPLICANT: Cytomed, Inc. (all states except US)
6      : APPLICANT: Nocka, Karl (US only)
7      : APPLICANT: Lobell, Robert B (US only)
8      : TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
9      : TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
10     : NUMBER OF SEQUENCES: 36
11     : CORRESPONDENCE ADDRESS:
12     : ADDRESSEE: Fish & Neave
13     : STREET: 1251 Avenue of the Americas
14     : CITY: New York
15     : STATE: New York
16     : COUNTRY: United States of America
17     : ZIP: 10020
18     : COMPUTER READABLE FORM:
19     : MEDIUM TYPE: Floppy disk
20     : COMPUTER: IBM PC compatible
21     : OPERATING SYSTEM: PC-DOS/MS-DOS
22     : SOFTWARE: Patentln Release #1.0, Version #1.30
23     : CURRENT APPLICATION DATA:
24     : APPLICATION NUMBER: PCT/US95/03866
25     : FILING DATE:
26     : CLASSIFICATION:
27     : PRIOR APPLICATION DATA:
28     : APPLICATION NUMBER: US 08/220,379
29     : FILING DATE: 28-MAR-1994
30     : ATTORNEY/AGENT INFORMATION:
31     : NAME: Haley Jr, James F
32     : REGISTRATION NUMBER: 27,794
33     : REFERENCE/DOCKET NUMBER: Cytomed/2
34     : TELECOMMUNICATION INFORMATION:
35     : TELEPHONE: 212-596-9000
36     : TELEFAX: 212-596-9090
37     : INFORMATION FOR SEQ ID NO: 14:
38     : SEQUENCE CHARACTERISTICS:
39     : LENGTH: 424 amino acids
40     : TYPE: amino acid
41     : TOPOLOGY: linear
42     : MOLECULE TYPE: protein
43     : PCT-US95-03866-14

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Query Match	97.2%	Score 1225;	DB 5;	Length 424;
Best Local Similarity	97.0%	Pred. No. 8.7e-116;		
Matches 225; Conservative	3;	Mismatches 4;	Indels 0;	Gaps 0;

Qy	1	EPKSCDKHTCCPCAPBELLGGPSFVFLPPPKKDTLMSTRPEYTCVVDVSHDEPKVF	60
Db	193	EPKSCDKHTCCPCAPBELLGGPSFVFLPPPKKDTLMSTRPEYTCVVDVSHDEPKVF	252
Qy	61	NMYVDGEVHNMYKTRKEBOYNSTRVYVSVLTVLHQMNMNGKEYKCKVSNKALPAPIEKT	120
Db	253	NMYVDGEVHNMYKTRKEBOYNSTRVYVSVLTVLHQMNMNGKEYKCKVSNKALPAPIEKT	312
Qy	121	ISKAKYQPREPOVYTLTPPSRDELTLNQVSLTCLVKGFPSPDIAMWESNGPENNYKTP	180
Db	313	ISKAKYQPREPOVYTLTPPSRDELTLNQVSLTCLVKGFPSPDIAMWESNGPENNYKTP	372
Qy	181	PVLDISGSGFFLYSKLTVDKSRWQOGNVFSCSYMEHAIHNHYQORSLSLSPEK	232
Db	373	PVLDISGSGFFLYSKLTVDKSRWQOGNVFSCSYMEHAIHNHYQORSLSLSPEK	424

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RESULT 14
PCT-US96-10043-11
; Sequence 11, Application PC/TUS9610043
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES

```



TITLE OF INVENTION: AND METHODS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02210-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10043  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,213  
FILING DATE: 14-JUN-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lech, Karen P.  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 00786/284001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 437 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-10043-11

Query Match 97.2%; Score 1235; DB 5; Length 437;  
Best Local Similarity 97.0%; Pred. No. 9.1e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPFPKPKDITLMISRTPEVTCVVDVSHEDPEVKF 60  
DB 206 EPKSCDKHTHTCPCPAPPELLGSPSVFLPFPKPKDITLMISRTPEVTCVVDVSHEDPEVKF 265  
QY 61 NMYVDGVEVHNAVTKYKPREQYNSTYRVSVLTVLHQNMMNGEYKCKVSNKALPAPIEKT 120  
DB 266 NMYVDGVEVHNAVTKYKPREQYNSTYRVSVLTVLHQNMMNGEYKCKVSNKALPAPIEKT 325  
QY 121 ISKAVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESGQPENNYKTP 180  
DB 326 ISKAVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESGQPENNYKTP 385  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYOQRSLSLSPGK 232  
DB 386 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYOQRSLSLSPGK 437

RESULT 15  
US-08-472-888A-7  
Sequence 7, Application US/08472888A  
Patent No. 6613746  
GENERAL INFORMATION:  
APPLICANT: Seed, Brian  
APPLICANT: Walz, Gerd  
TITLE OF INVENTION: AGP-ANTIBODY FUSION PROTEINS  
TITLE OF INVENTION: AND RELATED MOLECULES AND METHODS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street

CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472, 888A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/618, 314  
FILING DATE: 23-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Elbing, Karen L.  
REGISTRATION NUMBER: 35, 238  
REFERENCE/DOCKET NUMBER: 00786/258001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 442 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-472-888A-7

Query Match 97.2%; Score 1225; DB 4; Length 442;  
Best Local Similarity 97.0%; Pred. No. 9.3e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPFPKPKDITLMISRTPEVTCVVDVSHEDPEVKF 60  
DB 211 EPKSCDKHTHTCPCPAPPELLGSPSVFLPFPKPKDITLMISRTPEVTCVVDVSHEDPEVKF 270  
QY 61 NMYVDGVEVHNAVTKYKPREQYNSTYRVSVLTVLHQNMMNGEYKCKVSNKALPAPIEKT 120  
DB 271 NMYVDGVEVHNAVTKYKPREQYNSTYRVSVLTVLHQNMMNGEYKCKVSNKALPAPIEKT 330  
QY 121 ISKAVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESGQPENNYKTP 180  
DB 331 ISKAVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESGQPENNYKTP 390  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYOQRSLSLSPGK 232  
DB 391 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYOQRSLSLSPGK 442

Search completed: June 7, 2005, 09:04:01  
Job time : 33.456 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: June 7, 2005, 08:48:08 ; Search time 1.79102 Seconds  
(without alignments)  
913.271 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94  
Sequence: 1 ENPVVHFFKNIVTPRTP 17Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summariesDatabase :  
1: p1r.79:.\*  
2: p1r2:.\*  
3: p1r3:.\*  
4: p1r4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	100.0	128	1 MBRTS	myelin basic prote
2	94	100.0	167	2 A37246	myelin basic prote
3	94	100.0	169	1 MBROB	myelin basic prote
4	94	100.0	171	1 MBPCB	myelin basic prote
5	94	100.0	171	1 MBPCB	myelin basic prote
6	94	100.0	197	1 MBHUB	myelin basic prote
7	94	100.0	328	1 MBMSB	goli-myelin basic
8	87	92.6	174	2 S08535	myelin basic prote
9	60	63.8	128	2 A60215	myelin basic prote
10	53	56.4	155	2 B32959	myelin basic prote
11	45	47.9	308	2 A57440	hypothetical prote
12	44	46.8	329	2 A57246	beta-tectorin prec
13	44	46.8	639	2 T46577	arylsulfatase (BC
14	43	45.7	14	2 S12804	protein kinase (EC
15	43	45.7	85	2 C89965	conserved hypothet
16	43	45.7	134	2 T28704	hypothetical prote
17	43	45.7	395	2 H72222	conserved hypothet
18	43	45.7	672	2 A11183	transcription regu
19	43	45.7	1124	2 B44742	probable receptor-
20	42	44.7	435	2 AB3076	glutamine syntheta
21	42	44.7	435	2 G98210	glutamine syntheta
22	42	44.7	435	2 JC1301	glutamate-ammonia
23	42	44.7	891	2 AG1541	similar to transcr
24	42	44.7	891	2 T40137	hypothetical serin
25	41	43.6	48	2 D82534	hypothetical prote
26	41	43.6	332	2 E70384	biotin synthase (E
27	41	43.6	480	2 A12308	cytochrome D ubiqu
28	41	43.6	646	2 A11174	internalin, probab
29	41	43.6	690	2 E84945	glycine-tRNA ligas

30	41	43.6	892	2 T27005	hypothetical prote
31	40	42.6	192	2 AD2530	hypothetical prote
32	40	42.6	428	2 D96934	cytosine/guanine d
33	40	42.6	431	2 T50177	probable peptide m
34	40	42.6	983	2 H72510	probable ribonuclease
35	40	42.6	1162	2 T51040	hypothetical prote
36	40	42.6	2089	2 C85426	ATM-like protein (
37	40	42.6	3738	2 T05501	hypothetical prote
38	39	41.5	164	2 F88690	glutamate racemase
39	39	41.5	250	2 B81262	hypothetical prote
40	39	41.5	270	2 F86897	hypothetical prote
41	39	41.5	323	2 T15311	hypothetical prote
42	39	41.5	333	2 S18578	C4-dicarboxylate-b
43	39	41.5	337	2 F89944	conserved hypothet
44	39	41.5	431	2 H70302	conserved hypothet
45	39	41.5	471	2 AB0308	o-succinylbenzoate

## ALIGNMENTS

## RESULT 1

MBRTS

myelin basic protein S - rat  
N/Alternate names: small myelin basic protein

C/Species: Rattus norvegicus (Norway rat)

C/Date: 24-Apr-1984 #sequence revision 08-Feb-1996 #ext\_change 09-Jul-2004

C/Accession: B24351; A90275; A94243; A21062; A03142

R/Schich, M.; Budzinski, R.M.; Stoffel, W.

Biol. Chem. Hoppe-Seyler 367, 825-834, 1986

A/Title: Cloned proteolipid protein and myelin basic protein cDNA. Transcription of the t

A/Reference number: A24351; UID:87026249; PMID:2429678

A/Accession: B24351

A/Molecule type: mRNA

A/Residues: 1-128 &lt;SCH&gt;

A/Cross-references: UNIPROT:P02688; EMBL:M25889; NID:G205321; PIDN:AAA41575.1; PID:G20532

R/Dunkley, P.R.; Carnegie, P.R.

Biochem. J. 141, 243-255, 1974

A/Title: Amino acid sequence of the smaller basic protein from rat brain myelin.

A/Reference number: A90275; UID:75127359; PMID:4141893

A/Accession: A90275

A/Molecule type: protein

A/Residues: 2-128 &lt;DUN&gt;

A/Note: at position 105, arginine, monomethylarginine, and dimethylarginine occur in the

A/Note: rats have two myelin basic proteins; the smaller one, shown above, is missing 40

R/McFarlin, D.E.; Blank, S.E.; Kibler, R.F.; McKeally, S.; Shapira, R.

Science 179, 478-480, 1973

A/Title: Experimental allergic encephalomyelitis in the rat: response to encephalitogenic

A/Reference number: A94243; UID:73180720; PMID:4122324

A/Accession: A94243

A/Molecule type: protein

A/Residues: 46-86 &lt;MCF&gt;

A/Note: the sequence reported for this encephalitogenic peptide differs from that shown t

R/Boach, A.; Boylan, K.; Horvath, S.; Prusiner, S.B.; Hood, L.B.

Cell 34, 799-806, 1983

A/Title: Characterization of cloned cDNA representing rat myelin basic protein: absence c

A/Reference number: A21062; UID:84026484; PMID:6194889

A/Accession: A21062

A/Molecule type: mRNA

A/Residues: 1-124, 126-128 &lt;ROA&gt;

A/Experimental source: strain Sprague-Dawley

C/Suprafamily: myelin basic protein

F/2-128/Product: myelin basic protein S #status experimental &lt;AT&gt;

F/2/Modified site: blocked amino end (Ala) (in mature form) (probably acetylated) #status

F/105/Modified site: omega-N-methylarginine or omega-N'-methylarginine (Arg) (if

Query Match 100.0%; Score 94; DB 1; Length 128;

Best local similarity 100.0%; Pred. No. 1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
|||||

Db 81 ENPVVHFFKNITVTPRTP 97

RESULT 2

A37246  
myelin basic protein - guinea pig

N:Alternate names: myelin A1 protein

C:Species: Cavia porcellus (guinea pig)

C:Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #ext\_change 09-Jul-2004

C:Accession: A37246; C92087; A03140

J:Deblater, G.E.; Martenson, R.E.; Kruttsch, H.C.; Kies, M.W.

J: Neurochem. 43, 100-105, 1984

A:Title: Sequence of guinea pig myelin basic protein.

A:Reference number: A37246; PMID:84215086; PMID:6202840

A:Accession: A37246

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-167 <DEI>

A:Cross-references: UNIPROT:P25188

R:Shapiro, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.

J: Biol. Chem. 246, 4630-4640, 1971

A:Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovin

A:Reference number: A92087

A:Accession: C92087

A:Molecule type: protein

A:Residues: 45-87 <SHA>

C:Superfamily: myelin basic protein

C:Keywords: myelin

Query Match 100.0%; Score 94; DB 2; Length 167;  
Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVHFFKNITVTPRTP 17  
|||||

Db 82 ENPVVHFFKNITVTPRTP 98

RESULT 3

MEBOB  
myelin basic protein - bovine

N:Alternate names: myelin A1 protein

C:Species: Bos primigenius taurus (cattle)

C:Date: 18-Dec-1981 #sequence\_revision 18-Dec-1981 #ext\_change 09-Jul-2004

C:Accession: A92089; A92160; A92087; S54343; A61641; B61641; A03140

R:Eylar, E.H.; Brostoff, S.; Hashim, G.; Caccam, J.; Burnett, P.

J: Biol. Chem. 246, 5770-5784, 1971

A:Title: Basic A1 protein of the myelin membrane. The complete amino acid sequence.

A:Reference number: A92089; PMID:72007306; PMID:5096093

A:Accession: A92089

A:Molecule type: protein

A:Residues: 1-'S',2-169 <EYL>

A:Cross-references: UNIPROT:P02687

R:Brostoff, S.W.; Reuter, W.; Hichens, M.; Eylar, E.H.

J: Biol. Chem. 249, 558-567, 1974

A:Title: Specific cleavage of the A1 protein from myelin with cathepsin D.

A:Reference number: A92160; PMID:74070688; PMID:4129204

A:Accession: A92160

A:Molecule type: protein

A:Residues: 1-169 <BRO>

R:Shapiro, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.

J: Biol. Chem. 246, 4630-4640, 1971

A:Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovin

A:Reference number: A92087

A:Accession: A92087

A:Molecule type: protein

A:Residues: 43-87 <SHA>

R:Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.

Biochem. J. 306, 551-555, 1995

A:Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in gli

A:Reference number: S54343; PMID:95194333; PMID:7887910

A:Accession: S54343

A:Molecule type: protein

A:Residues: 74-75,'HG',78-82,'D',84-88,105,'X',107-108,'X',110-114,'X',116-119 <OKA>

R:Yakamatsu, K.; Iatenco, K.

Neurochem. Res. 17, 239-246, 1992

A:Title: Isolation and characterization of two novel peptide amides originating from mye

A:Reference number: A61641; PMID:92319189; PMID:1377792

A:Accession: A61641

A:Molecule type: protein

A:Residues: 1-112 <TK>

A:Accession: B61641

A:Molecule type: protein

A:Residues: 1-16 <TA2>

A:Note: these peptides have carboxyl-terminal amides probably produced by a non-enzymatic

R:Brostoff, S.; Eylar, E.H.

Proc. Natl. Acad. Sci. U.S.A. 68, 765-769, 1971

A:Title: Localization of methylated arginine in the A1 protein from myelin.

A:Reference number: A93777; PMID:71153946; PMID:4994464

A:Contents: annotation

A:Note: Arg-106 is modified to monomethylarginine and dimethylarginine

R:Eylar, E.H.; Caccam, J.; Jackson, J.J.; Westall, P.C.; Robinson, A.B.

Science 168, 1220-1223, 1970

A:Title: Experimental allergic encephalomyelitis: synthesis of disease-inducing site of t

A:Reference number: A94241; PMID:70178977; PMID:5442707

A:Contents: annotation

A:Note: the region including residues 114-122 induces experimental allergic encephalomyel

C:Superfamily: myelin basic protein

C:Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune encephal

F:1-169/Product: myelin basic protein #status experimental <MAT>

F:1-16/Product: myelin peptide amide-16 #status experimental <PA16>

F:1-12/Product: myelin peptide amide-12 #status experimental <PA12>

F:12/Modified site: acetylated amino end (Ala) #status experimental

F:12/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide amic

F:16/Modified site: amidated carboxyl end (Ala) (amide in mature form myelin peptide amic

F:106/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg) (f

Query Match 100.0%; Score 94; DB 1; Length 169;  
Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVHFFKNITVTPRTP 17  
|||||

Db 82 ENPVVHFFKNITVTPRTP 98

RESULT 4

MECZB  
myelin basic protein - chimpanzee (tentative sequence)

N:Alternate names: MBP

C:Species: Pan troglodytes (chimpanzee)

C:Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #ext\_change 09-Jul-2004

C:Accession: A03139

R:Westall, P.C.; Thompson, M.; Katter, S.S.

Life Sci. 17, 219-223, 1975

A:Title: The proposed sequence of the encephalitogenic protein from chimpanzee brain.

A:Reference number: A03139; PMID:76009821; PMID:51459

A:Accession: A03139

A:Molecule type: protein

A:Residues: 1-171 <WES>

A:Cross-references: UNIPROT:P06906

C:Comment: This protein may function in maintaining the proper structure of myelin.

C:Superfamily: myelin basic protein

C:Keywords: blocked amino end; methylated amino acid; myelin; structural protein

F:1/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental

F:107/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg) #

Query Match 100.0%; Score 94; DB 1; Length 171;  
Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVHFFKNITVTPRTP 17  
|||||

Db 83 ENPVHFFKNITVTPRTP 99

RESULT 5  
MBPG  
myelin basic protein - pig (tentative sequence)  
N:Alternate names: myelin A1 protein  
N:Contains: myelin basic protein amide 14  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 19-Apr-1996 #sequence\_\_revision 26-Apr-1996 #text\_change 09-Jul-2004  
C:Accession: A61640; A66245  
R:Kira, J.; Delbler, G.E.; Krutzsch, H.C.; Martenson, R.E.  
J. Neurochem. 44, 134-142, 1985  
A:Title: Amino acid sequence of porcine myelin basic protein.  
A:Reference number: A61640; MUID:85056964; PMID:2578056  
A:Accession: A61640  
A:Molecule type: protein  
A:Residues: 1-171 <KIR>  
A:Cross-references: UNIPROT:P81558  
A:Note: some peptides were ordered by homology  
R:Takamatsu, K.; Tatemoto, K.  
Biochem. Biophys. Res. Commun. 172, 1167-1174, 1990  
A:Title: Isolation and characterization of a novel peptide amide from porcine brain.  
A:Reference number: A36245; MUID:91058553; PMID:1700904  
A:Accession: A36245  
A:Molecule type: protein  
A:Residues: 1-14 <TRK>  
A:Note: the sequence in the abstract is inconsistent with that in figure 3 in having Glu  
A:Note: this peptide has a carboxyl-terminal amide probably produced by a non-enzymatic  
C:Superfamily: myelin basic protein  
C:Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune encephalomyelitis  
F:1-171/Product: myelin basic protein #status experimental <MAT>  
F:1-14/Product: myelin peptide amide-14 #status experimental <PA12>  
F:1/Modified site: acetylated amino end (Ala) #status experimental  
F:14/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide amide  
F:107/Modified site: omega-N-methylarginine or omega-N, omega-N'-dimethylarginine (Arg)

Query Match 100.0%; Score 94; DB 1; Length 171;  
Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVHFFNIVTPRP 17  
|||  
Db 83 ENPVHFFNIVTPRP 99

RESULT 6  
MBHUB  
myelin basic protein (validated) - human  
N:Contains: myelin basic protein precursor, 17.2K splice form; myelin basic protein precursor, 5K splice form  
C:Species: Homo sapiens (man)  
C:Date: 18-Dec-1981 #sequence\_revision 25-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: S10483; A94106; B94106; A90255; JH0802; A60862; A61420; A33273; I54219; I56  
R:Streicher, R.; Scofield, W.  
Biochem. Biophys. Res. Commun. 172, 503-510, 1989  
A:Title: The organization of the human myelin basic protein gene. Comparison with the mouse  
A:Reference number: S10483; MUID:89302693; PMID:2472816  
A:Accession: S10483  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-197 <STR>  
A:Cross-references: UNIPROT:P02666; EMBL:X17286; MUID:G34490; PIDN:CMA35179.1; PID:G11842  
R:Kamholz, J.; De Ferreira, P.; Puckett, C.; Lazzerini, R.  
Proc. Natl. Acad. Sci. U.S.A. 83, 4962-4966, 1986  
A:Title: Identification of three forms of human myelin basic protein by cDNA cloning.  
A:Reference number: A94106; MUID:86259714; PMID:2425357  
A:Accession: A94106  
A:Molecule type: mRNA  
A:Residues: 1-59, 86-197 <RAM>  
A:Cross-references: GB:M13577; NID:G187408; PIDN:AAA59562.1; PID:G307160  
A:Note: 18.5K splice form  
A:Accession: B94106  
A:Molecule type: mRNA  
A:Residues: 1-197 <KA2>

A:Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form  
A:Note: a 17.2K splice form is also described  
A:Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form; a 17.2K sp  
R:Carnegie, P.R.  
Biochem. J. 123, 57-67, 1971  
A:Title: Amino acid sequence of the encephalitogenic basic protein from human myelin.  
A:Reference number: A90256; MUID:72066400; PMID:4108501  
A:Accession: A90256  
A:Molecule type: protein  
A:Residues: 2-59, 86-197 <CAR>  
R:Proost, P.; Van Damme, J.; Opdenacker, G.  
Biochem. Biophys. Res. Commun. 192, 1175-1181, 1993  
A:Title: Leukocyte gelatinase B cleavage releases encephalitogens from human myelin basic  
A:Reference number: JH0802; MUID:93282820; PMID:7685161  
A:Accession: JH0802  
A:Molecule type: protein  
A:Residues: 2-59, 86-197 <PRO>  
A:Experimental source: brain  
R:Scoble, H.A.; Whitaker, J.N.; Biemann, K.  
J. Neurochem. 47, 614-616, 1986  
A:Title: Analysis of the primary sequence of human myelin basic protein peptides 1-44 and  
A:Reference number: A60862; MUID:86280476; PMID:2426402  
A:Accession: A60862  
A:Molecule type: protein  
A:Residues: 2-45, 117-197 <SCO>  
A:Note: evidence for acetylated amino end  
R:Gibson, B.W.; Gilliom, R.D.; Whitaker, J.N.; Biemann, K.  
J. Biol. Chem. 259, 5028-5031, 1984  
A:Title: Amino acid sequence of human myelin basic protein peptide 45-89 as determined by  
A:Reference number: A61420; MUID:84185608; PMID:6201481  
A:Accession: A61420  
A:Molecule type: protein  
A:Residues: 46-59, 86-116 <GIB>  
R:Wood, D.D.; Moscarello, M.A.  
J. Biol. Chem. 264, 5121-5127, 1989  
A:Title: The isolation, characterization, and lipid-aggregating properties of a citrullin  
A:Reference number: A33273; MUID:89174797; PMID:2466844  
A:Accession: A33273  
A:Molecule type: protein  
A:Residues: 15-25, 'X', 27-31, 'X', 33-59, 86-148, 'X', 150-156, 'X', 158-185, 'X', 187-196, 'X' <MO<  
A:Note: form C-8; residues designated 'X' were determined as citrulline  
R:Balwin, G.S.; Carnegie, P.R.  
Biochem. J. 123, 69-74, 1971  
A:Title: Isolation and partial characterization of methylated arginines from the encephal  
A:Reference number: A90257; MUID:72066401; PMID:5128665  
A:Contents: annotation; methylarginine  
A:Note: Arg-134 may be unmodified, monomethylarginine, or dimethylarginine in the approxi  
R:Lennon, V.A.; Wilks, A.V.; Carnegie, P.R.  
J. Immunol. 105, 1223-1230, 1970  
A:Reference number: A92806; MUID:71088405; PMID:4099924  
A:Contents: annotation  
A:Note: a region including residues 139-149 induces experimental autoimmune encephalomyel  
R:Boylan, K.B.; Ayres, T.W.; Popko, B.; Takahashi, N.; Hood, L.E.; Prineas, S.B.  
Genomics 6, 16-22, 1990  
A:Title: Repetitive DNA (TGCAG)n 5' to the human myelin basic protein gene: a new form of  
A:Reference number: I54219; MUID:90152679; PMID:1689270  
A:Accession: I54219  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-59 <RES>  
A:Cross-references: GB:M63599; NID:G187402; PIDN:AAA59560.1; PID:G187403  
R:Booth, H.J.; Kronquist, K.R.; Keriato de Rosbo, N.; Crandall, B.F.; Campagnoni, A.T.  
J. Neurosci. Res. 17, 321-328, 1987  
A:Title: Evidence for the expression of four myelin basic protein variants in the develop  
A:Reference number: I56567; MUID:87711781; PMID:2442403  
A:Accession: I56567  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-132, 144-197 <RES>  
A:Cross-references: GB:M30516; NID:G187410; PIDN:AAA59563.1; PID:G307161  
A:Accession: I73634  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA

A:Residues: 1-197 <RE3>  
A:Cross-references: GB:M30515; NID:G187412; PIDN:AAA59564.1; PID:G307162  
R:Roach, H.J.; Kronquist, K.; Precorius, P.J.; Crandall, B.F.; Campagnoni, A.T.  
J. Neurosci. Res. 16, 227-238, 1986  
A:Title: Isolation and characterization of a cDNA coding for a novel human 17.3K myelin  
A:Reference number: 156565; MUID:86308101; PMID:2427738  
A:Accession: 156565  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-59, 86-133, 145-197 <RE4>  
A:Cross-references: GB:M30047; NID:G187400; PIDN:AAA59559.1; PID:G307159  
R:Bouliac, C.; Pang, H.; Mastroianni, F.; Moscarello, M.A.  
Arch. Biochem. Biophys. 332, 174-182, 1995  
A:Title: The isolation and characterization of four myelin basic proteins from the unbo  
A:Reference number: S66383; MUID:96004793; PMID:7574672  
A:Accession: S66383  
A:Molecule type: protein  
A:Residues: 23-25, 'X', 27-39 <BOU>  
C:Comment: Four alternatively spliced forms of myelin basic protein have been observed.  
C:Gene: GDB:MBP  
A:Cross-references: GDB:119379; OMIM:159430  
A:Map position: 18q22-18qter  
A:Introns: 59/3; 85/3; 120/3; 132/3; 143/3; 183/3  
C:Function:  
A:Description: probably helps maintain myelin structure  
C:Superfamily: myelin basic protein  
C:Keywords: acetylated amino end; alternative splicing; citrulline; experimental autoimm  
F:2-197/Product: myelin basic protein, 21.5K splice form #status predicted <MAT1>  
F:2-132,144-197/Product: myelin basic protein, 20.2K splice form #status predicted <MAT2  
F:2-59,86-137/Product: myelin basic protein, 18.5K splice form #status experimental <MAT  
F:2-59,86-132,144-197/Product: myelin basic protein, 17.2K splice form #status predicted  
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental  
F:26,32,149,157,186,197/Modified site: citrulline (Arg) (in form C-8) #status experim  
F:134/Modified site: omega-N-methylarginine or omega-N-dimethylarginine (Arg) (

Query Match 100.0%; Score 94; DB 1; Length 197;  
Best Local Similarity 100.0%; Pred. No. 1.7e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNITVPTPT 17  
110 ENPVVHFFKNITVPTPT 126  
Db

RESULT 7  
MEMSB  
goli1-myelin basic protein precursor - mouse  
N:Alternate names: goli1-mbp protein; MBP  
N:Contents: myelin basic protein  
C:Species: Mus musculus (house mouse)  
C:Dates: 17-Mar-1987 #sequence revision 07-Oct-1994 #text change 09-Jul-2004  
A:Accession: A45421; B45421; A90867; A26591; B26591; A60920; 148407; 158996; 154  
R:Campagnoni, A.T.; Pribyl, T.M.; Campagnoni, C.W.; Kampf, K.; Amur-Umarjee, S.; Landry,  
J. Biol. Chem. 268, 4930-4938, 1993  
A:Title: Structure and developmental regulation of Goli1-mbp, a 105-kilobase gene that e  
A:Reference number: A45421; MUID:93186801; PMID:7680345  
A:Accession: A45421  
A:Molecule type: mRNA  
A:Residues: 1-190,217-276,316-328 <CAN1>  
A:Cross-references: UNIPROT:P04370; GB:L07507; NID:G193584  
A:Experimental source: clone J37  
A:Note: sequence extracted from NCBI backbone (NCBIN:126696) and modified  
A:Accession: B45421  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-191, 'SSEP' <CAN2>  
A:Cross-references: GB:L07508; NID:G193586; PIDN:AAA7721.1; PID:G193587  
A:Experimental source: clone BG21  
A:Note: sequence extracted from NCBI backbone (NCBIN:126700, NCBI:126725)  
R:de Ferra, F.; Engh, H.; Hudson, L.; Kamholz, J.; Puckett, C.; Molinaux, S.; Lazzarini  
Cell 43, 721-727, 1985

A:Title: Alternative splicing accounts for the four forms of myelin basic protein.  
A:Reference number: A90875; MUID:86079555; PMID:2416470  
A:Accession: A90875  
A:Molecule type: mRNA  
A:Residues: 134-328 <DEF>  
A:Cross-references: GB:L00404; GB:M1669; NID:G199060; PIDN:AAA39502.1; PID:G387419  
R:Experimental source: 21.5K  
R:Itakashi, N.; Roach, A.; Tephlow, D.B.; Prusiner, S.B.; Hood, L.  
Cell 42, 139-148, 1985  
A:Title: Cloning and characterization of the myelin basic protein gene from mouse: one ge  
A:Reference number: A90867; MUID:85254913; PMID:2410136  
A:Accession: A90867  
A:Molecule type: DNA  
A:Residues: 134-190,217-328 <TAK>  
A:Cross-references: GB:M1533; NID:G199044; PIDN:AAA39496.1; PID:G387414  
A:Experimental source: 18.5K  
R:Newman, S.; Kitamura, K.; Campagnoni, A.T.  
Proc. Natl. Acad. Sci. U.S.A. 84, 886-890, 1987  
A:Title: Identification of a cDNA coding for a fifth form of myelin basic protein in mou  
A:Reference number: A9188; MUID:87118269; PMID:2433693  
A:Accession: A26591  
A:Molecule type: mRNA  
A:Residues: 134-274,316-328 <NEM1>  
A:Cross-references: GB:M15060; NID:G199048; PIDN:AA59711.1; PID:G199049  
A:Experimental source: clone M722; splice form 17.22K  
A:Accession: B26591  
A:Molecule type: mRNA  
A:Residues: 134-190,217-263,275-328 <NEM2>  
A:Cross-references: GB:M15063; NID:G199050  
A:Experimental source: clone M78; splice form 17.24K  
R:Kitamura, K.; Newman, S.L.; Campagnoni, C.W.; Verdi, J.M.; Mohandae, T.; Handley, V.W.;  
J. Neurochem. 54, 2032-2041, 1990  
A:Title: Expression of a novel transcript of the myelin basic protein gene.  
A:Reference number: A60920; MUID:90250449; PMID:1692584  
A:Accession: A60920  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 134-190,217-274,316-328 <KIT>  
A:Experimental source: M41; splice form 14K  
R:Grima, B.; Zelenika, D.; Pessac, B.  
J. Neurochem. 59, 2318-2323, 1992  
A:Title: A novel transcript overlapping the myelin basic protein gene.  
A:Reference number: 148407; MUID:93057537; PMID:1279125  
A:Accession: 148407  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-191, 'SSEP' <GRI>  
A:Cross-references: EMBL:X67319; NID:G51332; PIDN:CAA47733.1; PID:G51333  
A:Note: submitted to the EMBL Data Library, July 1992  
R:Zeller, N.K.; Hunkeler, M.J.; Campagnoni, A.T.; Sprague, J.; Lazzarini, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 81, 18-22, 1984  
A:Title: Characterization of mouse myelin basic protein messenger RNAs with a myelin bas  
A:Reference number: 158996; MUID:84119431; PMID:1596644  
A:Accession: 158996  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 219-248 <ZEL>  
A:Cross-references: GB:X00989; NID:G199037; PIDN:AAA39495.1; PID:G54195  
R:Miura, M.; Tamura, T.  
Gene 75, 31-38, 1989  
A:Title: The promoter elements of the mouse myelin basic protein gene function efficientl  
A:Reference number: 154033; MUID:89252919; PMID:2470651  
A:Accession: 154033  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 134-157 <MU>  
A:Cross-references: GB:M24410; NID:G199052; PIDN:AAA39498.1; PID:G554196  
R:Okano, H.; Tamura, T.; Miura, M.; Aoyama, A.; Ikenaka, K.; Oshimura, M.; Mikoshiba, K.  
EMBO J. 7, 77-83, 1988  
A:Title: Gene organization and transcription of duplicated MBP genes of myelin deficient  
A:Reference number: 153256; MUID:88196094; PMID:2452084  
A:Accession: 153256  
A:Status: translation not shown; translated from GB/EMBL/DBJ

A.Molecule type: DNA  
A.Residues: 217-229, 'NN', 232-250 <OKA>  
A.Cross-references: GB:M36275; NID:G199069; PIDN:AAA9504.1; PID:G293725  
A.Note: Hypothetical translation of the reversed and complementary sequence to that shown  
C.Comment: Mice have five forms of myelin basic protein: 21.5K, 18.5K, 17.24K, 17.22K and  
C.Genetics:  
A.Gene: Goll1-mbp, shi-mld  
A.Introns: 190/3; 250/3; 262/3; 273/3; 314/3  
C.Function:  
A.Description: probably helps maintain myelin structure  
C.Superfamily: myelin basic protein  
C.Keywords: alternative splicing; myelin; structural protein  
F:1-190, 217-276, 316-328/Product: Goll1-mbp protein (clone J37) #status predicted <MA1>  
F:134-328/Product: myelin basic protein, splice form 21.5K #status predicted <MA1>  
F:134-274, 316-328/Product: myelin basic protein, splice form 17K-a #status predicted <MA1>  
F:134-190, 217-276, 316-328/Product: myelin basic protein, splice form 18.5K #status predicted <MA1>  
F:134-190, 217-276, 316-328/Product: myelin basic protein, splice form 17K-b #status predicted <MA1>  
F:134-190, 217-274, 316-328/Product: myelin basic protein, splice form 14K #status predicted <MA1>

Query Match 100.0%; Score 94; DB 1; Length 328;  
Best Local Similarity 100.0%; Pred. No. 3e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVTPRP 17  
DB 240 ENPVVHFFKNITVTPRP 256

RESULT 8  
S08535  
myelin basic protein - chicken  
C.Species: Gallus gallus (chicken)  
C.Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #ext\_change 09-Jul-2004  
C.Accession: S08535  
R:Zopf, D.; Somte, V.; Betz, H.; Gundelfinger, E.D.  
G:1-2, 241-249, 1989  
A.Title: Developmental accumulation and heterogeneity of myelin basic protein transcript  
A.Reference number: S08535; MUID:89358239; PMID:2475444  
A.Accession: S08535  
A.Molecule type: mRNA  
A.Residues: 1-174 <ZOP>  
A.Cross-references: UNIPROT:P15720; EMBL:X17103; NID:G63594; PIDN:CAA4959.1; PID:G63595  
C.Superfamily: myelin basic protein

Query Match 92.6%; Score 87; DB 2; Length 174;  
Best Local Similarity 88.2%; Pred. No. 2.3e-07;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVTPRP 17  
DB 82 DNPVHFFKNITVTPRP 98

RESULT 9  
A60215  
myelin basic protein - dusky shark (fragments)  
C.Species: Carcharias obscurus (dusky shark)  
C.Date: 10-Nov-1992 #sequence\_revision 12-Mar-1993 #ext\_change 09-Jul-2004  
C.Accession: A60215  
R:Milne, T.J.; Atkins, A.R.; Warren, J.A.; Auton, W.P.; Smith, R.  
J. Neurochem. 55, 950-955, 1990  
A.Title: Shark myelin basic protein: amino acid sequence, secondary structure, and self-  
A.Reference number: A60215; MUID:90347402; PMID:1696624  
A.Accession: A60215  
A.Molecule type: protein  
A.Residues: 1-128 <MIL>  
A.Cross-references: UNIPROT:P98190  
A.Note: the source was designated as Carcharias obscurus (whaler shark)  
C.Superfamily: myelin basic protein

Query Match 63.8%; Score 60; DB 2; Length 128;  
Best Local Similarity 52.9%; Pred. No. 0.0065;  
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVTPRP 17  
DB 46 DSAVHFFKNITVTPRP 62

RESULT 10  
B32999  
myelin basic protein - horn shark  
C.Species: Heterodontus francisci (horn shark)  
C.Date: 21-Feb-1990 #sequence\_revision 21-Feb-1990 #ext\_change 09-Jul-2004  
C.Accession: B32999  
R:Saavedra, R.A.; Fors, L.; Aebersold, R.H.; Arden, B.; Horvath, S.; Sanders, J.; Hood, L.  
J. Mol. Evol. 29, 149-156, 1989  
A.Title: The myelin proteins of the shark brain are similar to the myelin proteins of the  
A.Reference number: A32999; MUID:90040744; PMID:2478717  
A.Accession: B32999  
A.Status: preliminary  
A.Molecule type: mRNA  
A.Residues: 1-155 <SAA>  
A.Cross-references: UNIPROT:P20939; GB:X17664; NID:G63974; PIDN:CAA35661.1; PID:G63975  
C.Superfamily: myelin basic protein

Query Match 56.4%; Score 53; DB 2; Length 155;  
Best Local Similarity 53.3%; Pred. No. 0.13;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVTPR 15  
DB 72 DSAVHFFKNITVTPR 86

RESULT 11  
G64440  
hypothetical protein MJ1128 - Methanococcus jannaschii  
C.Species: Methanococcus jannaschii  
C.Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #ext\_change 09-Jul-2004  
C.Accession: G64440  
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.;  
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodok, A.;  
Ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hult, M.A.  
Science 273, 1058-1073, 1996  
A.Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
A.Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.  
A.Reference number: A64300; MUID:96337999; PMID:8688087  
A.Accession: G64440  
A.Status: preliminary; nucleic acid sequence not shown; translation not shown  
A.Molecule type: DNA  
A.Residues: 1-308 <BUL>  
A.Cross-references: UNIPROT:Q58528; GB:U67555; GB:L77117; NID:G1591760; PIDN:AAB99130.1;  
C.Genetics:  
A.Map position: REV1069975-1069049  
A.Start codon: GTG  
C.Superfamily: hypothetical protein MJ1128

Query Match 47.9%; Score 45; DB 2; Length 308;  
Best Local Similarity 70.0%; Pred. No. 6.7;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ENPVVHFFKN 10  
DB 35 ENPVVHFFKN 44

RESULT 12  
A57246  
beta-lectorin precursor - chicken  
C.Species: Gallus gallus (chicken)  
C.Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #ext\_change 09-Jul-2004  
C.Accession: A57246  
R:Killick, R.; Legan, P.K.; Malenczak, C.; Richardson, G.P.  
J. Cell Biol. 129, 535-547, 1995  
A.Title: Molecular cloning of chick beta-lectorin, an extracellular matrix molecule of ct



A:Reference number: A57246; MUID:95238547; PMID:7721949  
A:Accession: A57246  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-329 <KIL>  
C:Cross-references: UNIPROT:P54097; GB:L38519; NID:G602439; PIDN:AAA92461.1; PID:G602440  
C:Keywords: extracellular matrix; membrane protein; phosphatidylinositol linkage

Query Match 46.8%; Score 44; DB 2; Length 329;  
Best Local Similarity 53.8%; Pred. No. 11;  
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ENPVVHFKNIVT 13  
DB 91 KNPVYHFVNSIVS 103

RESULT 13  
T46577  
arylsulfatase (EC 3.1.6.1) [validated] - Neurospora crassa  
C:Species: Neurospora crassa  
C:Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 09-Jul-2004  
C:Accession: T46577  
R:Baker, D.L.; Paletta, J.V.  
A:Description: Molecular characterization of the arylsulfatase gene of Neurospora crassa  
A:Reference number: Z23090  
A:Accession: T46577  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-639 <BAK>  
A:Cross-references: UNIPROT:O43113; EMBL:U89492; PIDN:AAC02716.1  
A:Experimental source: strain wild type 74-OR23-1A  
C:Genetics:  
A:Gene: ars-1  
A:Map position: 7  
A:Introns: 115/1; 518/3  
C:Function:  
A:Description: EC 3.1.6.1 [validated, MUID:89384589]  
A>Note: genes are expressed under conditions of sulfur limitation and are under coordin  
C:Superfamily: plant sulfatase  
C:Keywords: sulfuric ester hydrolase

Query Match 46.8%; Score 44; DB 2; Length 639;  
Best Local Similarity 50.0%; Pred. No. 23;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 HFFKNIVTPRT 17  
DB 282 HFFPVIVPRT 293

RESULT 14  
S12904  
protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)  
C:Species: Pisaster ochraceus  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S12904  
R:Sanghera, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.  
FEBS Lett. 273, 223-226, 1990  
A:Title: Identification of the sites in myelin basic protein that are phosphorylated by  
A:Reference number: S12904; MUID:91032186; PMID:1699809  
A:Accession: S12904  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <SAN>  
A:Cross-references: UNIPROT:Q7M3M4  
C:Keywords: phosphotransferase

Query Match 45.7%; Score 43; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.41;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NIVTPRT 17  
DB 1 NIVTPRT 8

RESULT 15  
C89965  
conserved hypothetical protein SA1613 [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: C89965  
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc  
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratake, K.  
Lancet 357, 1225-1240, 2001  
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A:Reference number: A89758; MUID:21311952; PMID:11418146  
A:Accession: C89965  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-85 <KUR>  
A:Cross-references: UNIPROT:Q99775; GB:BA000018; PID:G13701588; PIDN:BA842881.1; GSPDB:G  
A:Experimental source: strain N315  
C:Genetics:  
A:Gene: SA1613  
C:Superfamily: conserved hypothetical protein H11000

Query Match 45.7%; Score 43; DB 2; Length 85;  
Best Local Similarity 35.7%; Pred. No. 3.3;  
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 4 VHFKNIVTPRT 17  
DB 8 MIFVQRFISPLTP 21

Search completed: June 7, 2005, 09:02:37  
Job time : 3.79102 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 08:39:41 ; Search time 8.36788 Seconds

(without alignments)  
1040.329 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94

Sequence: 1 ENPVVHFFKNIVTPRTP 17

Scoring table: BLOSUM62

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	74	2	Q6A164
2	94	100.0	158	2	Q8R4K6
3	94	100.0	160	2	Q6F104
4	94	100.0	167	1	MBP_CAVPO
5	94	100.0	168	1	MBP_RABIT
6	94	100.0	169	1	MBP_BOVIN
7	94	100.0	171	1	MBP_PANTR
8	94	100.0	171	1	MBP_PIG
9	94	100.0	173	2	Q6J2R3
10	94	100.0	180	2	Q6PK23
11	94	100.0	194	1	MBP_RAT
12	94	100.0	203	2	Q6S2S4
13	94	100.0	250	1	MBP_MOUSE
14	94	100.0	304	1	MBP_HUMAN
15	87	92.6	173	1	MBP_CHICK
16	84	89.4	175	1	MBP_XENLA
17	78	83.0	172	1	MBP_HORSE
18	61	64.9	154	1	MBP_RAUER
19	61	64.9	154	1	MBP_SQUAC
20	60	63.8	128	2	P98190
21	53	56.4	154	1	MBP_HETFR
22	49.5	52.7	300	2	Q6B1Z9
23	47	50.0	300	2	Q6B1Z9
24	47	50.0	669	2	Q6DB87
25	46	48.9	440	2	Q881D3
26	46	48.9	1529	2	Q7ZX12
27	45	47.9	308	1	YB28_MERUA
28	45	47.9	322	2	Q7V1H9
29	45	47.9	441	2	Q965U5
30	45	47.9	759	2	Q8EE95
31	44	46.8	215	2	Q7RJU7

32	44	46.8	329	1	TECB_CHICK	P54097 gallus galli
33	44	46.8	334	2	Q6N857	Q6N857 rhodopseudo
34	44	46.8	398	2	Q84H45	Q84H45 clostridium
35	44	46.8	501	2	Q7RJU8	Q7RJU8 plasmodium
36	44	46.8	527	2	Q6KHL8	Q6KHL8 mycoplasma
37	44	46.8	618	2	Q86ZNS	Q86ZNS podospira a
38	44	46.8	639	2	Q43113	Q43113 neurospora
39	44	46.8	639	2	Q7RV09	Q7RV09 neurospora
40	43	45.7	14	2	Q7M3M4	Q7M3M4 pisaster oc
41	43	45.7	85	1	YG13_STRAN	P67305 staphylococ
42	43	45.7	85	1	YH33_STRAM	P67304 staphylococ
43	43	45.7	85	1	YH33_STRAM	P67304 staphylococ
44	43	45.7	85	1	Q6G8D8	Q6G8D8 staphylococ
45	43	45.7	85	2	Q6GFR2	Q6GFR2 staphylococ

## ALIGNMENTS

RESULT 1					
ID	Q6A164	PRELIMINARY;	PRT;	74 AA.	
AC	Q6A164				
DT	25-OCT-2004 (TREMBLrel. 28, Created)				
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)				
DE	Hypothetical protein DKFZp6810845 (Fragment).				
GN	Name=DKFZp6810845;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OC	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Amygdala;				
RG	The German CDNA Consortium;				
RA	Ottewaelde B., Obermayer B., Deutschenbaur S., Schaipp A.,				
RA	Mewes H.W., Weill B., Amlid C., Osanger A., Fobo G., Han M., Wiemann S.;				
RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; CR627018; CAH10359.1; -				
DR	GO; GO:0019911; F:Structural constituent of myelin sheath; IEA.				
DR	InterPro; IPR000548; Myelin_BP.				
DR	Pfam; PF01669; Myelin_BP; 1.				
DR	ProDom; PD004542; Myelin_BP; 1.				
KW	PROSITE; PS00569; MYELIN_MBP; 1.				
KW	Hypothetical protein.				
FT	NON_TER				
SQ	SEQUENCE 74 AA; 8265 MW; ACFE96ACBE9AE551 CRC64;				
Query Match					
Best Local Similarity 100.0%; Score 94; DB 2; Length 74;					
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 ENPVVHFFKNIVTPRTP 17				
DB	41 ENPVVHFFKNIVTPRTP 57				
RESULT 2					
ID	Q8R4K6	PRELIMINARY;	PRT;	158 AA.	
AC	Q8R4K6				
DT	01-JUN-2002 (TREMBLrel. 21, Created)				
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)				
DE	Myelin basic protein.				
GN	Name=Mbp;				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OC	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				

```

RC STRAIN=Sprague-Dawley;
RX MEDLINE=22941925; PubMed=14580679; DOI=10.1016/j.bbaexp.2003.08.010;
RA Mathews L., Blair G.E.;
RT "Identification and characterization of a cDNA encoding a 17-kDa
RL isoform of rat myelin basic protein.";
RN Biochim. Biophys. Acta 1630:47-53(2003).
RP [12]
RR SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Mathews L.M., Blair G.E.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF439750; AAL84189.1; -
DR GO: GO:0019911; F:structural constituent of myelin sheath; IEA.
DR InterPro: IPR000548; Myelin_BP.
DR Pfam: PF01669; Myelin_MBP; I.
DR PRINTS; PR00212; MYELINMBP.
DR ProDom; PD004542; MYELINBP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
SQ SEQUENCE 158 AA; 17240 MW; 3256580242EC3E1 CRC64;

Query Match 100.0%; Score 94; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVTPRP 17
DB 81 ENPVVHFFKNITVTPRP 97

RESULT 3
06FI04 PRELIMINARY; PRT; 160 AA.
AC 06FI04;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE MBP protein.
GN Name=MBP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Ketrang K., Schalten R., Shen B., Henze S., War W.,
RA Korn B., Zuo D., Hu Y., Labaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR536534; CAG38771.1; -
DR GO: GO:0019911; F:structural constituent of myelin sheath; IEA.
DR InterPro: IPR000548; Myelin_BP.
DR Pfam; PF01669; Myelin_MBP; 1.
DR PRINTS; PR00212; MYELINMBP.
DR ProDom; PD004542; MYELINBP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
SQ SEQUENCE 160 AA; 17347 MW; 0107AD6053CD876 CRC64;

Query Match 100.0%; Score 94; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVTPRP 17
DB 84 ENPVVHFFKNITVTPRP 100

RESULT 4
MBP_CAVPO STANDARD; PRT; 167 AA.
ID MBP_CAVPO
AC P25188;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
PT
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DE Myelin basic protein (MBP).
GN Name=MBP;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.
OX NCB1_TaxId=10141;
RN [1]
RR SEQUENCE.
RP MEDLINE=84215086; PubMed=6202840;
RA Deliber G.E., Martenson R.E., Krutzsch H.C., Kies M.W.;
RT "Sequence of guinea pig myelin basic protein.";
RL J. Neurochem. 43:100-105 (1984).
RN [2]
RR SEQUENCE OF 7-156 FROM N.A.
RC STRAIN=Hartley; TISSUE=Spinal cord;
RA Kim G., Tanuma N., Matsumoto Y.;
RT "DNA vaccination using Guinea pig myelin basic protein coding region
RL in experimental autoimmune encephalomyelitis.";
RN Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RR SEQUENCE OF 45-87.
RA Shapira R., McKernally S.S., Chou F., Kibler R.F.;
RT "Encephalitogenic fragment of myelin basic protein. Amino acid
RL sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
RN J. Biol. Chem. 246:4630-4640(1971).
RN [4]
RR POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=76025020; PubMed=51849;
RA Deliber G.E., Martenson R.E., Kramer A.J., Kies M.W.;
RT "The contribution of phosphorylation and loss of COOH-terminal
RL arginine to the microheterogeneity of myelin basic protein.";
RN J. Biol. Chem. 250:7931-7938(1975).
CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the
CC myelin membrane in the CNS. Has a role in both the formation and
CC stabilization of this compact multilayer arrangement of bilayers.
CC Each splice variant and charge isomer may have a specialized
CC function in the assembly of an optimized, biochemically functional
CC myelin membrane (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
CC -1- TISSUE SPECIFICITY: Found in both the central and the peripheral
CC nervous system.
CC -1- PTM: At least 5 charge isomers; C1 (the most cationic, least
CC modified, and most abundant form), C2, C3, C4 and C5 (the least
CC cationic form); are produced as a result of optional
CC posttranslational modifications such as phosphorylation of serine
CC or threonine residues, deamidation of glutamine or asparagine
CC residues, citrullination and methylation of arginine residues. C1
CC and C2 are unphosphorylated, C3 and C4 are monophosphorylated and
CC C5 is phosphorylated at two positions.
CC -1- SIMILARITY: Belongs to the myelin basic protein family.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AF074337; AAC26130.1; -
DR F01; A37246; A37246.
DR HSSP; P02686; 1QCL.
DR InterPro; IPR000548; Myelin_BP.
DR Pfam; PF01669; Myelin_MBP; 1.
DR PRINTS; PR00212; MYELINMBP.
DR ProDom; PD004542; MYELINBP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
DR Acetylation; Autoimmune encephalomyelitis; Citrullination;
DR Direct protein sequencing; Methylation; Myelin; Phosphorylation;
DR Structural protein.
FT DOMAIN 45 87
FT Induces experimental autoimmune
FT encephalomyelitis (EAE) 1.
```

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FT DOMAIN 114 122 Induces experimental autoimmune
FT MOD_RES 1 1 encephalomyelitis (EAE) 2.
FT MOD_RES 7 7 N-acetylgalactamine.
FT MOD_RES 25 25 Phosphoserine (By similarity).
FT MOD_RES 31 31 Citrulline (By similarity).
FT MOD_RES 56 56 Citrulline (By similarity).
FT MOD_RES 97 97 Phosphothreonine (By similarity).
FT MOD_RES 102 102 Phosphothreonine (By similarity).
FT MOD_RES 106 106 Deamidated glutamine (partial) (By
FT MOD_RES 114 114 similarity).
FT MOD_RES 129 129 Symmetric dimethylarginine (By
FT MOD_RES 144 144 phosphoserine (By similarity).
FT MOD_RES 144 144 Citrulline (By similarity).
FT MOD_RES 156 156 Deamidated glutamine (partial) (By
FT MOD_RES 158 158 similarity).
FT MOD_RES 162 162 Citrulline (By similarity).
FT MOD_RES 167 167 Phosphoserine (By similarity).
SQ SEQUENCE 167 AA; 18213 MW; 866D31F1E5ACFEA6 CRC64;

Query Match 100.0%; Score 94; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17
Db 82 ENPVVHFFKNIVTPRTP 98

RESULT 5
MBP_RABIT STANDARD; PRT; 168 AA.
AC P25734;
DT 01-MAY-1992 (Rel. 22, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Myelin basic protein (MBP) (Myelin P1 protein).
GN Name=MBP;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RP PRELIMINARY SEQUENCE.
RC TISSUE=Sciatic nerve;
RA MEDLINE=73190037; PubMed=4662101;
RA Brostoff S.W., Eylar E.H.;
RT "The proposed amino acid sequence of the P1 protein of rabbit sciatic
RT nerve myelin."
RL Arch. Biochem. Biophys. 153:590-598(1972).
RN [2]
RN SEQUENCE OF 45-86.
RP Shapira R., McKnearly S.S., Chou F., Kibler R.F.;
RA "Encephalogenic fragment of myelin basic protein. Amino acid
RA sequence of bovine, rabbit, guinea pig, monkey, and human fragments."
RT J. Biol. Chem. 246:4630-4640(1971).
RN [3]
RN PHOSPHORYLATION.
RP MEDLINE=83108902; PubMed=6185481;
RA Martenson R.E., Law M.J., Deblor G.E.;
RT "Identification of multiple in vivo phosphorylation sites in rabbit
RT myelin basic protein."
RL J. Biol. Chem. 258:930-937(1983).
RN [4]
RN FUNCTION: Is, with PIP, the most abundant protein component of the
RN myelin membrane in the CNS. Has a role in both the formation and
RN stabilization of this compact multilayer arrangement of bilayers.
RN Each splice variant and charge isomer may have a specialized
RN function in the assembly of an optimized, biochemically functional
RN myelin membrane (By similarity).
RN -1- SUBUNIT: Homodimer (By similarity).
RN -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.

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CC -1- TISSUE SPECIFICITY: Found in both the central and the peripheral
CC nervous system.
CC -1- PTM: As in other animals, several charge isomers may be produced
CC as a result of optional posttranslational modifications, such as
CC phosphorylation of serine or threonine residues, deamidation of
CC glutamine or asparagine residues, citrullination and methylation
CC of arginine residues.
CC -1- PTM: The N-terminus is blocked.
CC -1- SIMILARITY: Belongs to the myelin basic protein family.
CC HSSP; P02686; 10CL.
DR InterPro: IPR000548; Myelin_Bp.
DR Pfam: PF01669; Myelin_MBP; I.
DR PRINTS: PR00212; MYELINBP.
DR ProDom: PD004542; Myelin_BP; 1.
DR PROSITE: PS00569; MYELIN_MBP; 1.
KW Acetylation; Autoimmune encephalomyelitis; Citrullination;
KW Direct protein sequencing; Methylation; Myelin; Phosphorylation;
KW Structural protein.
FT DOMAIN 45 86 Induces experimental autoimmune
FT MOD_RES 1 1 encephalomyelitis (EAE).
FT MOD_RES 7 7 N-acetylgalactamine (Probable).
FT MOD_RES 25 25 Phosphoserine.
FT MOD_RES 31 31 Citrulline (By similarity).
FT MOD_RES 31 31 Citrulline (By similarity).
FT MOD_RES 56 56 Phosphoserine.
FT MOD_RES 96 96 Phosphothreonine.
FT MOD_RES 101 101 Deamidated glutamine (partial)
FT MOD_RES 105 105 (Probable).
FT MOD_RES 105 105 Omega-N-methylarginine (partial).
FT MOD_RES 105 105 Symmetric dimethylarginine (partial).
FT MOD_RES 113 113 Phosphoserine.
FT MOD_RES 128 128 Citrulline (By similarity).
FT MOD_RES 145 145 Deamidated glutamine (partial) (By
FT MOD_RES 157 157 similarity).
FT MOD_RES 157 157 Citrulline (By similarity).
FT MOD_RES 159 159 Phosphoserine (By similarity).
FT MOD_RES 163 163 Phosphoserine.
FT MOD_RES 168 168 Citrulline (By similarity).
FT MOD_RES 168 168 Citrulline (By similarity).
SQ SEQUENCE 168 AA; 18217 MW; EC3C97ACD2C08EA6 CRC64;

Query Match 100.0%; Score 94; DB 1; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17
Db 81 ENPVVHFFKNIVTPRTP 97

RESULT 6
MBP_BOVIN STANDARD; PRT; 169 AA.
ID MBP_BOVIN
AC P02687; Q9BGM8; Q9TS63; Q9TS66;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Myelin basic protein (MBP) (Myelin A1 protein) (20 kDa microtubule
DE stabilizing protein).
GN Name=MBP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RN SEQUENCE.
RP MEDLINE=72007306; PubMed=5096093;
RA Eylar E.H., Brostoff S.W., Hashim G., Caccam J., Burnett P.;
RT "Basic A1 protein of the myelin membrane. The complete amino acid
RT sequence."
RL J. Biol. Chem. 246:5770-5784(1971).
RN [2]

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RP REVISION.  
RX MEDLINE=74070688; PubMed=4129204;  
RA Brostoff S.W., Reuter W., Hichens M., Eylar E.H.;  
RT "Specific cleavage of the A1 protein from myelin with cathepsin D.";  
RL J. Biol. Chem. 249:559-567(1974).  
[3]  
RP SEQUENCE OF 4-56 FROM N.A.  
RA Piotrowski D., Medugorac I., Foerster M.;  
RT "A new MBP allele in Bos taurus is characterized by BseI PCR-RFLP";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
[4]  
RP SEQUENCE OF 43-87.  
RA Shapira R., McKneally S.S., Chou F.C.-H., Kibler R.F.;  
RT "Encephalitogenic fragment of myelin basic protein. Amino acid  
sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";  
RL J. Biol. Chem. 246:4630-4640(1971).  
[5]  
RP SEQUENCE OF 38-58 AND 119-141.  
RA TISSUE=Brain;  
RX MEDLINE=9303019; PubMed=1382581;  
RA Pirolier F., Derancourt J., Hache J., Job D., Margolis R.L.;  
RT "Ca(2+)-calmodulin regulated effectors of microtubule stability in  
bovine brain.";  
RL Biochemistry 31:8849-8855(1992).  
[6]  
RP SEQUENCE OF 30-42; 74-89 AND 114-129.  
RX MEDLINE=96107211; PubMed=8530487; DOI=10.1074/jbc.270.51.30551;  
RA Praad K., Barouch W., Martin B.M., Greene L.E., Eisenberg E.;  
RT "Purification of a new clathrin assembly protein from bovine brain  
coated vesicles and its identification as myelin basic protein.";  
RL J. Biol. Chem. 270:30551-30556(1995).  
[7]  
RP SYNTHESIS OF ALLERGIC ENCEPHALOMYELITIS INDUCING REGION.  
RX MEDLINE=70178977; PubMed=5442707;  
RA Eylar E.H., Caccam J., Jackson J.J., Westall F.C., Robinson A.B.;  
RT "Experimental allergic encephalomyelitis: synthesis of disease-  
inducing site of the basic protein.";  
RL Science 168:1220-1223(1970).  
[8]  
RP METHYLATION.  
RX MEDLINE=71153946; PubMed=4994464;  
RA Brostoff S.W., Eylar E.H.;  
RT "Localization of methylated arginine in the A1 protein from myelin.";  
RL Proc. Natl. Acad. Sci. U.S.A. 68:765-769(1971).  
[9]  
RP POST-TRANSLATIONAL MODIFICATIONS.  
RX MEDLINE=76167591; PubMed=57115;  
RA Chou F.C.-H., Chou C.-H.J., Shapira R., Kibler R.F.;  
RT "Basis of microheterogeneity of myelin basic protein.";  
RL J. Biol. Chem. 251:2671-2679(1976).  
[10]  
RP SEQUENCE OF 97-104, AND PHOSPHORYLATION SITE THR-97.  
RX MEDLINE=91060584; PubMed=1700979;  
RA Erickson A.K., Payne D.M., Marcino P.A., Rosomando A.J.,  
RA Shanonowicz J., Weber M.J., Hunt D.F., Sturgill T.W.;  
RT "Identification by mass spectrometry of threonine 97 in bovine myelin  
basic protein as a specific phosphorylation site for mitogen-activated  
protein kinase.";  
RL J. Biol. Chem. 265:19728-19735(1990).  
[11]  
RP POST-TRANSLATIONAL MODIFICATIONS.  
RX MEDLINE=98153125; PubMed=9485392; DOI=10.1021/bj972347c;  
RA Zand R., Li M.X., Jin X., Lubman D.;  
RT "Determination of the sites of posttranslational modifications in the  
chargin isomers of bovine myelin basic protein by capillary  
electrophoresis-mass spectroscopy.";  
RL Biochemistry 37:2441-2449(1998).  
[12]  
RP DIMERIZATION.  
RX MEDLINE=80198320; PubMed=6155143;  
RA Smith R.;  
RT "Sedimentation analysis of the self-association of bovine myelin basic  
protein.";

RL Biochemistry 19:1826-1831(1980).  
CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the  
CC myelin membrane in the CNS. Has a role in both the formation and  
CC stabilization of this compact multilayer arrangement of bilayers.  
CC Each splice variant and charge isomer may have a specialized  
CC function in the assembly of an optimized, biochemically functional  
CC myelin membrane (By similarity).  
CC -1- SUBUNIT: Homodimer; self-associates in the presence of lysolipid.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.  
CC -1- TISSUE SPECIFICITY: Found in both the central and the peripheral  
CC nervous system.  
CC -1- PTM: At least 6 charge isomers; C1 (the most cationic and least  
CC modified form), C2, C3, C4, C5 and C6 (the least cationic form);  
CC are produced as a result of optional posttranslational  
CC modifications, such as phosphorylation of serine or threonine  
CC residues, deamidation of glutamine or asparagine residues,  
CC citrullination and methylation of arginine residues.  
CC -1- SIMILARITY: Belongs to the myelin basic protein family.  
CC -----  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
CC EMBL; AF226693; AAK00645.1; -  
CC PIR; A92089; MBOB.  
CC HSPSP; P02686; 10CL.  
CC InterPro: IPR000548; Myelin BP.  
CC Pfam: PF01669; Myelin MBP; I.  
CC PRINTS; PR00212; MYELINBP.  
CC ProDom; PD004542; Myelin BP; 1.  
CC PROSITE; PS00569; MYELIN MBP; 1.  
CC Acetylglutamine: Autoimmune encephalomyelitis; Citrullination;  
CC Direct protein sequencing; Methylation; Myelin; Phosphorylation;  
CC Structural protein.  
CC KW  
CC DOMAIN 43 87  
CC FT  
CC DOMAIN 114 122  
CC FT  
CC MOD\_RES 1 1  
CC FT MOD\_RES 7 7  
CC FT MOD\_RES 23 23  
CC FT MOD\_RES 29 29  
CC FT MOD\_RES 54 54  
CC FT MOD\_RES 97 97  
CC FT  
CC MOD\_RES 102 102  
CC FT MOD\_RES 106 106  
CC FT MOD\_RES 106 106  
CC FT MOD\_RES 114 114  
CC FT MOD\_RES 129 129  
CC FT MOD\_RES 146 146  
CC FT MOD\_RES 158 158  
CC FT MOD\_RES 160 160  
CC FT MOD\_RES 164 164  
CC FT MOD\_RES 169 169  
CC SQ SEQUENCE 169 AA; 18323 MW; 8E1157B7A1978484 CRC64;  
Query Match 100.0%; Score 94; DB 1; Length 169;  
Best local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
Db 82 ENPVVHFFKNIVTPRTP 98  
RESULT 7  
MBP\_PANTR  
ID\_MBP\_PANTR STANDARD; PRT; 171 AA.

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AC P06906;
DT 01-JAN-1988 (rel. 06, Created)
DT 01-JAN-1988 (rel. 06, Last sequence update)
DR 25-OCT-2004 (rel. 45, Last annotation update)
DE Myelin basic protein (MBP).
GN Name=MBP;
OS Pan troglodytes (chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OC NCBI_TaxID=9598;
OX [1]
RN PRELIMINARY SEQUENCE.
RP MEDLINE=76009821; PubMed=51459; DOI=10.1016/0024-3205(75)90506-8;
RX Westall F.C., Thompson M., Katter S.S.;
RT "The proposed sequence of the encephalitogenic protein from chimpanzee
  brain."
RL Life Sci. 17:219-223(1975).
CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the
CC myelin membrane in the CNS. Has a role in both the formation and
CC stabilization of this compact multilayer arrangement of bilayers.
CC Each splice variant and charge isomer may have a specialized
CC function in the assembly of an optimized, biochemically functional
CC myelin membrane (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
CC -1- PTM: As in other animals, several charge isomers may be produced
CC as a result of optional posttranslational modifications, such as
CC phosphorylation of serine or threonine residues, deamidation of
CC glutamine or asparagine residues, citrullination and methylation
CC of arginine residues.
CC -1- SIMILARITY: Belongs to the myelin basic protein family.
CC PIR: A01139; MBOCB.
DR HSSP; P02686; IQCL.
DR InterPro; IPR000548; Myelin_BP.
DR Pfam; PF00212; MYELINBP.
DR PRINTS; PR004542; Myelin_BP.1.
DR PROSITE; PS00569; MYELIN_BP.1.
KW Acetylation; Autoimmune encephalomyelitis; Citrullination;
KW Direct protein sequencing; Methylation; Myelin; Phosphorylation;
KW Structural protein.
FT MOD_RES 1 1 N-acetylalanine.
FT MOD_RES 7 7 Phosphoserine (By similarity).
FT MOD_RES 25 25 Citrulline (By similarity).
FT MOD_RES 31 31 Citrulline (By similarity).
FT MOD_RES 56 56 Phosphoserine (By similarity).
FT MOD_RES 98 98 Phosphothreonine (By similarity).
FT MOD_RES 103 103 Deamidated glutamine (partial) (By
  similarity).
FT MOD_RES 107 107 Omega-N-methylated arginine.
FT MOD_RES 115 115 Phosphoserine (By similarity).
FT MOD_RES 122 122 Citrulline (By similarity).
FT MOD_RES 130 130 Citrulline (By similarity).
FT MOD_RES 148 148 Deamidated glutamine (partial) (By
  similarity).
FT MOD_RES 160 160 Citrulline (By similarity).
FT MOD_RES 162 162 Phosphoserine (By similarity).
FT MOD_RES 166 166 Phosphoserine (By similarity).
FT MOD_RES 171 171 Citrulline (By similarity).
SQ SEQUENCE 171 AA; 18560 MW; E9FED59DE633293 CRC64;

Query Match 100.0%; Score 94; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
DB 83 ENPVVHFFKNIVTPRTP 99

RESULT 8
MBP_PIG STANDARD; PRT; 171 AA.
ID MBP_PIG

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AC P81558; P98189;
DT 30-MAY-2000 (rel. 39, Created)
DT 30-MAY-2000 (rel. 39, Last sequence update)
DR 05-JUL-2004 (rel. 44, Last annotation update)
DE Myelin basic protein (MBP).
GN Name=MBP;
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OC NCBI_TaxID=9823;
OX [1]
RN SEQUENCE, AND METHYLATION OF ARG-107.
RP TISSUE=Brain;
RX MEDLINE=85056964; PubMed=2578056;
RX Kira J.-I., Delbier G.E., Krutzsch H.C., Martenson R.E.;
RT "Amino acid sequence of porcine myelin basic protein."
RL J. Neurochem. 44:134-142(1985).
RN [2]
RP ERRATUM.
RA Kira J.-I., Delbier G.E., Krutzsch H.C., Martenson R.E.;
RL J. Neurochem. 44:1663-1663(1985).
CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the
CC myelin membrane in the CNS. Has a role in both the formation and
CC stabilization of this compact multilayer arrangement of bilayers.
CC Each splice variant and charge isomer may have a specialized
CC function in the assembly of an optimized, biochemically functional
CC myelin membrane (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
CC -1- PTM: As in other animals, several charge isomers may be produced
CC as a result of optional posttranslational modifications, such as
CC phosphorylation of serine or threonine residues, deamidation of
CC glutamine or asparagine residues, citrullination and methylation
CC of arginine residues.
CC -1- SIMILARITY: Belongs to the myelin basic protein family.
CC PIR: A61640; MBPG.
DR HSSP; P02686; IQCL.
DR InterPro; IPR000548; Myelin_BP.
DR Pfam; PF01669; MYELIN_BP.1.
DR PRINTS; PR00212; MYELINBP.
DR PROSITE; PS00569; MYELIN_BP.1.
DR PRODOM; PD004542; Myelin_BP.1.
KW Acetylation; Citrullination; Direct protein sequencing; Methylation;
KW Myelin; Phosphorylation; Structural protein.
FT MOD_RES 1 1 N-acetylalanine.
FT MOD_RES 7 7 Phosphoserine (By similarity).
FT MOD_RES 25 25 Citrulline (By similarity).
FT MOD_RES 31 31 Citrulline (By similarity).
FT MOD_RES 55 55 Phosphoserine (By similarity).
FT MOD_RES 98 98 Phosphothreonine (By similarity).
FT MOD_RES 103 103 Deamidated glutamine (partial) (By
  similarity).
FT MOD_RES 107 107 Omega-N-methylarginine (partial).
FT MOD_RES 107 107 Symmetric dimethylarginine (partial).
FT MOD_RES 115 115 Phosphoserine (By similarity).
FT MOD_RES 130 130 Citrulline (By similarity).
FT MOD_RES 148 148 Deamidated glutamine (partial) (By
  similarity).
FT MOD_RES 160 160 Citrulline (By similarity).
FT MOD_RES 162 162 Phosphoserine (By similarity).
FT MOD_RES 166 166 Phosphoserine (By similarity).
FT MOD_RES 171 171 Citrulline (By similarity).
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Query Match 100.0%; Score 94; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
DB 83 ENPVVHFFKNIVTPRTP 99

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DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DE Myelin basic protein.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim J.G., Noneman D., Vallet J.L., Rohrer G.A., Christenson R.K.;
RA Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY603684; AAT28338.1;
DR GO; GO:0019911; F:structural constituent of myelin sheath; IEA.
DR InterPro; IPR000548; Myelin BP.
DR Pfam; PF01669; Myelin_MBP; I.
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DR ProDom; PD004542; Myelin_BP; 1.
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SQ SEQUENCE 173 AA; 18731 MW; 6684D01E66081AA CRC64;

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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 85 ENPVVFFKNIVTPRT 101
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DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
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GN Name=MBP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Skin;
RA MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schaller G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ushed T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Kettlemen M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.

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RC TISSUE=Skin;
RA Strausberg R.;
RA Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC008749; AA08749.2;
DR GO; GO:0019911; F:structural constituent of myelin sheath; IEA.
DR InterPro; IPR000548; Myelin BP.
DR Pfam; PF01669; Myelin_MBP; I.
DR PRINTS; PR00212; MYELINMBP.
DR ProDom; PD004542; Myelin_BP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
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Query Match 100.0%; Score 94; DB 2; Length 180;
Best Local Similarity 100.0%; Fred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 93 ENPVVFFKNIVTPRT 109
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AC P02688; Q9Z1J4; Q9Z1J5; Q9Z1J6;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Myelin basic protein s (MBP S).
GN Name=MBP;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
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RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
RA Lobell A.M., Wiggall H.;
RA Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RA MEDLINE=87026249; PubMed=2429678;
RA Schach M., Budzinski R.M., Stofel W.;
RA "Cloned proteolipid protein and myelin basic protein cDNA.
RA Transcription of the two genes during myelination.";
RA Biol. Chem. Hoppe-Seyler 367:825-834(1986).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RA MEDLINE=84026484; PubMed=6194889; DOI=10.1016/0092-8674(83)90536-6;
RA Roach A., Boylan K.B., Horvath S., Prusiner S.B., Hood L.E.;
RA "Characterization of cloned cDNA representing rat myelin basic
RA protein: absence of expression in brain of shiverer mutant mice.";
RA Cell 34:799-806(1983).
RN [4]
RP SEQUENCE (ISOFORM 4).
RA MEDLINE=75127359; PubMed=4141893;
RA Dunkley P.R., Carnegie P.R.;
RA "Amino acid sequence of the smaller basic protein from rat brain
RA myelin.";
RA Biochem. J. 141:243-255(1974).
RN [5]
RP SEQUENCE OF 130-194 FROM N.A.
RA STRAIN=Lewis; TISSUE=Brain;
RA MEDLINE=96078224; PubMed=7578863;
RA Malocka J., Dormair K.;
RA "Alternative splicing and cDNA sequence of myelin basic protein gene
RA of the Lewis rat.";
RA Autoimmunity 20:67-68(1995).
RN [6]
RP SEQUENCE OF 45-111 (ISOFORM 4).
RA MEDLINE=73180720; PubMed=4122324;
RA McFarlin D.E., Blank S.E., Kibler R.F., McKeally S.S., Shapiro R.;
RA "Experimental allergic encephalomyelitis in the rat: response to

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## OM protein - protein search, using sw model

Run on: June 7, 2005, 09:01:44 ; Search time 7.45769 Seconds  
(without alignments)  
821.093 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94

Sequence: 1 ENPVVHFFKNIVTPRP 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 1599520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	94	100.0	17	US-10-104-973-3	Sequence 3, Appl1
2	94	100.0	17	US-10-000-439-13	Sequence 13, Appl1
3	94	100.0	17	US-10-362-264-1	Sequence 1, Appl1
4	94	100.0	17	US-10-233-892A-2	Sequence 2, Appl1
5	94	100.0	17	US-10-482-044-5	Sequence 5, Appl1
6	94	100.0	19	US-09-740-003-2	Sequence 2, Appl1
7	94	100.0	19	US-09-768-872-1	Sequence 1, Appl1
8	94	100.0	19	US-09-768-378A-32	Sequence 32, Appl1
9	94	100.0	19	US-10-239-313A-143	Sequence 143, Appl1
10	94	100.0	19	US-10-743-398-2	Sequence 2, Appl1
11	94	100.0	20	US-09-766-378A-28	Sequence 28, Appl1
12	94	100.0	20	US-09-836-433-30	Sequence 30, Appl1

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	16	94	100.0	23	9	US-09-909-460-1	Sequence 1, Appl1
	17	94	100.0	23	11 <td>US-09-872-836-1</td> <td>Sequence 1, Appl1</td>	US-09-872-836-1	Sequence 1, Appl1
	18	94	100.0	24	15 <td>US-10-149-138-4219</td> <td>Sequence 4219, Ap</td>	US-10-149-138-4219	Sequence 4219, Ap
	19	94	100.0	24	15 <td>US-10-149-135-2206</td> <td>Sequence 2206, Ap</td>	US-10-149-135-2206	Sequence 2206, Ap
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	22	94	100.0	46	9 <td>US-09-813-463A-1</td> <td>Sequence 1, Appl1</td>	US-09-813-463A-1	Sequence 1, Appl1
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## ALIGNMENTS

RESULT 1

US-10-104-973-3

Sequence 3, Application US/10104973

Publication No. US20020176866A1

GENERAL INFORMATION:

APPLICANT: Gaur, Amitabh

APPLICANT: Conlon, Paul J.

APPLICANT: Ling, Nicholas C.

APPLICANT: Staehlin, Theophil

TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING

TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN

FILE REFERENCE: 690068.405C4

CURRENT APPLICATION NUMBER: US/10/104,973

CURRENT FILING DATE: 2002-03-20

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 17

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Solid Phase

US-10-104-973-3

Query Match 100.0%; Score 94; DB 13; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.6e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRP 17

DB 1 ENPVVHFFKNIVTPRP 17

RESULT 2  
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; Sequence 13, Application US/10000439  
; Publication No. US20030064063A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES  
; FILE REFERENCE: UC067.004A  
; CURRENT APPLICATION NUMBER: US/10/000,439  
; PRIOR FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 09/847,208  
; PRIOR FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 13  
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; ORGANISM: Homo sapiens  
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DB 1 ENPVVHFFKNIVTPRTP 17

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; Sequence 1, Application US/10362264  
; Publication No. US20030191063A1  
; GENERAL INFORMATION:  
; APPLICANT: Wraith, David  
; APPLICANT: Anderton, Stephen  
; APPLICANT: Mazza, Graziella  
; APPLICANT: Ponsford, Mary  
; APPLICANT: Streeter, Heather  
; APPLICANT: The University of Bristol  
; TITLE OF INVENTION: PEPTIDE SELECTION METHOD  
; FILE REFERENCE: 1433.004US1  
; CURRENT APPLICATION NUMBER: US/10/362,264  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/GB01/03702  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 0020618.5  
; PRIOR FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: 0114547.3  
; PRIOR FILING DATE: 2001-06-14  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 1  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-362-264-1

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; Sequence 2, Application US/10233892A  
; Publication No. US20040043431A1  
; GENERAL INFORMATION:

; APPLICANT: Vojdani, Aristo  
; TITLE OF INVENTION: DIAGNOSIS OF MULTIPLE SCLEROSIS AND  
; TITLE OF INVENTION: OTHER DEMYELINATING DISEASES  
; FILE REFERENCE: IMSMS.001A  
; CURRENT APPLICATION NUMBER: US/10/233,892A  
; CURRENT FILING DATE: 2002-08-29  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 2  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Human Myelin Binding Protein Sequence 83-89  
US-10-233-892A-2

Query Match 100.0%; Score 94; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
| | | | | | | | | | | | | | | | | | |  
DB 1 ENPVVHFFKNIVTPRTP 17

RESULT 5  
US-10-482-044-5  
; Sequence 5, Application US/10482044  
; Publication No. US20040235713A1  
; GENERAL INFORMATION:  
; APPLICANT: Anna Maria PAPINI et al  
; TITLE OF INVENTION: Glycopeptides, their preparation and use in the diagnosis or  
; TITLE OF INVENTION: therapeutic treatment of multiple sclerosis  
; FILE REFERENCE: 2784 PTWO  
; CURRENT APPLICATION NUMBER: US/10/482,044  
; CURRENT FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: PCT/EP 02/06767  
; PRIOR FILING DATE: 2002-06-19  
; PRIOR APPLICATION NUMBER: FI2001A000114  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 5  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: glycopeptide  
; NAME/KEY: CARBOHYD  
; LOCATION: (2)..(2)  
; OTHER INFORMATION: the carbohydrate is beta-D-glucopyranosyl  
US-10-482-044-5

Query Match 100.0%; Score 94; DB 16; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
| | | | | | | | | | | | | | | | | | |  
DB 1 ENPVVHFFKNIVTPRTP 17

RESULT 6  
US-09-740-003-2  
; Sequence 2, Application US/09740003  
; Publication No. US20020039582A1  
; GENERAL INFORMATION:  
; APPLICANT: RAYCHAUDHURI, SYAMAL  
; APPLICANT: RASTETTER, WILLIAM H.  
; APPLICANT: BLACK, AMELIA  
; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES  
; FILE REFERENCE: 37003/275802

CURRENT APPLICATION NUMBER: US/09/740,003  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 09/024,220  
; PRIOR FILING DATE: 1998-02-17  
; PRIOR APPLICATION NUMBER: 08/476,674  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/351,001  
; PRIOR FILING DATE: 1994-12-07  
; PRIOR APPLICATION NUMBER: 08/919,787  
; PRIOR FILING DATE: 1997-08-29  
; PRIOR APPLICATION NUMBER: 07/735,069  
; PRIOR FILING DATE: 1991-07-25  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-740-003-2

Query Match 100.0%; Score 94; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ENPVHFFKNIVTPRTP 17  
Db 2 ENPVHFFKNIVTPRTP 18

RESULT 7  
US-09-768-872-1  
; Sequence 1, Application US/09768872  
; Patent No. US20020055466X1  
; GENERAL INFORMATION:  
; APPLICANT: Anaroni, Rina  
; APPLICANT: Teitelbaum, Dvora  
; APPLICANT: Arnon, Ruth  
; APPLICANT: Sela, Michael  
; APPLICANT: Fridkis-Harell, Masha  
; APPLICANT: Strominger, Jack  
; TITLE OF INVENTION: Treatment of Autoimmune Conditions with Copolymer 1  
; FILE REFERENCE: 1662/493762  
; CURRENT APPLICATION NUMBER: US/09/768,872  
; CURRENT FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: US 60/093,859  
; PRIOR FILING DATE: 1998-07-23  
; PRIOR APPLICATION NUMBER: US 60/101,825  
; PRIOR FILING DATE: 1998-09-25  
; PRIOR APPLICATION NUMBER: US 60/102,960  
; PRIOR FILING DATE: 1998-10-02  
; PRIOR APPLICATION NUMBER: US 60/106,350  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: US 60/108,184  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/123,675  
; PRIOR FILING DATE: 1999-03-09  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 1  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide (MBP residues 84-102)  
US-09-768-872-1

Query Match 100.0%; Score 94; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ENPVHFFKNIVTPRTP 17  
Db 2 ENPVHFFKNIVTPRTP 18

RESULT 8  
US-09-766-378A-32  
; Sequence 32, Application US/09766378A  
; Patent No. US20020091079X1  
; GENERAL INFORMATION:  
; APPLICANT: Rhode, Peter R.  
; Acevedo, Jorge  
; Burkhardt, Martin  
; Jiao, Jin-an  
; Wong, Hing C.  
; TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/766,378A  
; FILING DATE: 19-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/960,190  
; FILING DATE: 29-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Corleas, Peter F.  
; REGISTRATION NUMBER: 33,860  
; REFERENCE/DOCKET NUMBER: 48002-DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-766-378A-32

Query Match 100.0%; Score 94; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ENPVHFFKNIVTPRTP 17  
Db 2 ENPVHFFKNIVTPRTP 18

RESULT 9  
US-10-239-313A-143  
; Sequence 143, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGUER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain

APPLICANT: GOETSCH, Liliane  
TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
FILE REFERENCE: 343 727 - US  
CURRENT APPLICATION NUMBER: US/10/239,313A  
CURRENT FILING DATE: 2002-09-19  
PRIOR APPLICATION NUMBER: FR 00/03711  
PRIOR FILING DATE: 2000-03-23  
PRIOR APPLICATION NUMBER: PCT 01/70772  
PRIOR FILING DATE: 2001-03-22  
NUMBER OF SEQ ID NOS: 697  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 143  
LENGTH: 19  
TYPE: PRF  
ORGANISM: Homo sapiens  
US-10-239-313A-143

Query Match 100.0%; Score 94; DB 14; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRP 17  
|||  
Db 1 ENPVVHFFKNIVTPRP 17

RESULT 10  
US-10-743-398-2  
Sequence 2, Application US/10743398  
Publication No. US2004019731A1  
GENERAL INFORMATION:  
APPLICANT: RAYCHAUDHURI, SYAMAL  
APPLICANT: RASETTER, WILLIAM H.  
APPLICANT: BLACK, AMELIA  
TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES  
FILE REFERENCE: 37003/307430  
CURRENT APPLICATION NUMBER: US/10/743,398  
CURRENT FILING DATE: 2003-12-23  
PRIOR APPLICATION NUMBER: 09/740,003  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 09/024,220  
PRIOR FILING DATE: 1998-02-17  
PRIOR APPLICATION NUMBER: 08/476,674  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/351,001  
PRIOR FILING DATE: 1994-12-07  
PRIOR APPLICATION NUMBER: 08/919,787  
PRIOR FILING DATE: 1997-08-29  
PRIOR APPLICATION NUMBER: 07/735,069  
PRIOR FILING DATE: 1991-07-25  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 19  
TYPE: PRF  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
peptide  
US-10-743-398-2

Query Match 100.0%; Score 94; DB 16; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRP 17  
|||  
Db 2 ENPVVHFFKNIVTPRP 18

RESULT 11

US-09-766-378A-28  
Sequence 28, Application US/09766378A  
Patent No. US20020091079A1  
GENERAL INFORMATION:  
APPLICANT: Rhode, Peter R.  
Acevedo, Jorge  
Burkhardt, Martin  
Jiao, Jin-an  
Wong, Hing C.  
TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND  
METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: usa  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/766,378A  
FILING DATE: 19-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/960,190  
FILING DATE: 28-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Corleiss, Peter F.  
REGISTRATION NUMBER: 33,860  
REFERENCE/DOCKET NUMBER: 48002-DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 28:  
US-09-766-378A-28

Query Match 100.0%; Score 94; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRP 17  
|||  
Db 3 ENPVVHFFKNIVTPRP 19

RESULT 12  
US-09-836-433-30  
Sequence 30, Application US/09836433  
Publication No. US20030049797A1  
GENERAL INFORMATION:  
APPLICANT: Yuki, Yoshikazu  
APPLICANT: Uda, Shigezo  
TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE  
FILE REFERENCE: NO. US20030049797A1 Assigned  
CURRENT APPLICATION NUMBER: US/09/836,433  
CURRENT FILING DATE: 2001-04-16  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 30  
LENGTH: 20

SQL Sequence 17 AA; Query Match 100.0%; Score 94; DB 7; Length 17; Best Local Similarity 100.0%; Pred. No. 6.1e-09; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
1 ENPVVHFFKNIVTPRTP 17

DB 1 ENPVVHFFKNIVTPRTP 17

RESULT 9  
ADK67704  
ID ADK67704 standard; peptide; 17 AA.  
AC ADK67704;  
XX  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX Human myelin basic protein peptide fragment MBP-1 (aa110-126).  
XX  
XX Human; myelin basic protein; vaccine; multiple sclerosis; T cell.  
XX  
XX Homo sapiens.  
XX  
XX WO2004015070-A2.  
XX  
XX 19-FEB-2004.  
XX  
XX 06-AUG-2003; 2003WO-US024548.  
XX  
XX 08-AUG-2002; 2002US-0402521P.  
XX  
XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX (OPEX-) OPEXA PHARM INC.  
XX  
XX Zhang JZ;  
XX  
XX WPI; 2004-180654/17.

PT Isolating one or more T cells specific for an antigen of interest  
PT comprises incubating a T cell sample with an antigen, useful for  
PT diagnosing or treating multiple sclerosis, psoriasis, thyroiditis,  
PT diabetes and rheumatoid arthritis.

PS Example 1; SEQ ID NO 1; 38pp; English.

CC The present invention is direct to methods of isolating antigen specific  
CC T cells, especially T cells specific for self or autoantigens. This  
CC comprises incubating a sample of T cells obtained from a patient with the  
CC antigen and selecting T cells that express one or more of first markers  
CC selected from CD69, CD4, CD25, CD36 and HLA-DR, and one or more second  
CC markers selected from interleukin-2, interferon-gamma, tumour necrosis  
CC factor alpha, interleukin-5, interleukin-10 and interleukin-12. The  
CC methods are useful for isolating autoreactive T cells which play a role  
CC in the pathogenesis of autoimmune diseases. The methods also permit the  
CC diagnosis of autoimmune disease as well as monitoring the progression of  
CC the disease and for monitoring the efficacy of treatment. The methods of  
CC allow the preparation of autologous T cell vaccines for the treatment of  
CC T cell related autoimmune diseases. Vaccine preparation involves the  
CC isolation of antigen-specific T cells optionally followed by culturing  
CC steps which allow the expansion of the population of isolated antigen-  
CC specific T cells. An example from the invention describes the isolation  
CC of myelin-reactive T cells for T cell vaccination. Peripheral blood  
CC mononuclear cells were isolated from the blood of multiple sclerosis  
CC patients and incubated with peptides comprising known immunodominant  
CC regions of 3 myelin proteins. These included the present peptide, which  
CC comprises amino acids 110-126 of human myelin basic protein. Cells were  
CC then selected for the expression of gene products indicative of activated  
CC T cells, and myelin-reactive T cells were propagated in culture. The  
CC methods and compositions of the invention are useful for the diagnosis  
CC and/or treatment of autoimmune diseases or T cell associated conditions  
CC such as multiple sclerosis, myasthenia gravis, psoriasis, systemic lupus

CC erythematous, autoimmune thyroiditis, Grave's disease, inflammatory  
CC bowel disease, diabetes and rheumatoid arthritis.

SQL Sequence 17 AA; Query Match 100.0%; Score 94; DB 8; Length 17; Best Local Similarity 100.0%; Pred. No. 6.1e-09; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
1 ENPVVHFFKNIVTPRTP 17

DB 1 ENPVVHFFKNIVTPRTP 17

RESULT 10  
ADL18291  
ID ADL18291 standard; peptide; 17 AA.  
AC ADL18291;  
XX  
XX  
XX 20-MAY-2004 (first entry)  
XX  
XX Human myelin basic protein (MBP), peptide #2.  
XX  
XX Demyelinating disease; neuron-specific antigen; human;  
XX myelin basic protein; MBP; myelin oligodendrocyte glycoprotein;  
XX myelin associated glycoprotein; MAG; proteolipid protein; PLP;  
XX small heat shock protein; transaldolase; glial fibrillary protein;  
XX S-100 protein; cross-reactive peptide; glutamate receptor;  
XX phosphodiesterase; multiple sclerosis.  
XX  
XX Homo sapiens.  
XX  
XX US2004043431-A1.  
XX  
XX 04-MAR-2004.  
XX  
XX 29-AUG-2002; 2002US-00233892.  
XX  
XX 29-AUG-2002; 2002US-00233892.  
XX  
XX (VOUD/) VOUDANT A.  
XX  
XX Vojdant A;  
XX  
XX WPI; 2004-313756/29.

PT Diagnosing likelihood and severity of demyelinating disease, by  
PT determining antibodies against neuron-specific antigen, comparing level  
PT of detected antibodies with normal level for detecting absence/likelihood  
PT of demyelinating disease.

PS Claim 6; SEQ ID NO 2; 27pp; English.

CC The present invention relates to a method of diagnosing the likelihood  
CC and severity of demyelinating diseases. The method involves determining  
CC antibodies against neuron-specific antigen in sample, comparing the level  
CC of antibodies with the normal level of antibodies, where normal level of  
CC antibodies for neuron-specific antigen indicate optimal conditions, lower  
CC than or higher than normal level of antibodies for the antigen indicate  
CC an absence of or a likelihood of demyelinating diseases, respectively.  
CC The neuron-specific antigen is chosen from myelin basic protein (MBP),  
CC myelin oligodendrocyte glycoprotein, myelin associated glycoprotein  
CC (MAG), proteolipid protein (PLP), small heat shock protein,  
CC transaldolase, glial fibrillary protein, S-100 protein, cross-reactive  
CC peptide from dietary protein, cross-reactive peptide from infectious  
CC agent, glutamate receptor, and phosphodiesterase. The immunoassay is an  
CC enzyme linked immunosorbent assay (ELISA) test. The method is useful for  
CC diagnosing the likelihood and severity of demyelinating diseases such as  
CC multiple sclerosis in a patient. The present sequence represents a  
CC peptide from human MBP.

SQL Sequence 17 AA;

Query Match 100.0%; Score 94; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ENPVVHFFKNIVTPRTP 17  
 |||||  
 DB 1 ENPVVHFFKNIVTPRTP 17

## RESULT 11

AAR44115  
 ID AAR44115 standard; peptide; 18 AA.

AC AAR44115;

DT 25-MAR-2003 (revised)

DT 09-MAY-1994 (first entry)

XX Human myelin basic protein residues 85-102.

XX hMBP; suppression; auto immune response; multiple sclerosis;  
 XX immunodominant epitope; T-cell proliferation; CD4; T-cells.

OS Homo sapiens.

FN WO9321222-A1.

PD 28-OCT-1993.

PF 09-APR-1993; 93WO-US003369.

PR 09-APR-1992; 92US-00865318.

XX (AUTO-) AUTOIMMUNE INC.

PA Weiner HL, Haefler DA, Miller A, Al-Sabbagh A;

XX WPI; 1993-351657/44.

PT New peptide(s) derived from human myelin basic protein - used for  
 PT suppressing auto-immune response, partic. in treating multiple sclerosis.

PS Claim 1, Page 29; 118pp; English.

XX The peptide represents residues 85-102 of human myelin basic protein  
 CC (hMBP). The fragment comprises an immunodominant epitope of hMBP which  
 CC was identified by overlapping 20-mer oligopeptide sequence analysis using  
 CC T-cell line assays. The peptide can be used to stop proliferation of  
 CC human T-cells specific for MBP or to elicit active suppression of such T-  
 CC cells. They are also used partic. for the treatment of multiple  
 CC sclerosis. The peptide is also useful for identifying CD4+ T-cells  
 CC reactive with MBP. See also AAR44114-25. (Updated on 25-MAR-2003 to  
 CC correct PN field.)

XX Sequence 18 AA;

Query Match 100.0%; Score 94; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ENPVVHFFKNIVTPRTP 17  
 |||||  
 DB 1 ENPVVHFFKNIVTPRTP 17

## RESULT 12

AAR95357  
 ID AAR95357 standard; peptide; 18 AA.

AC AAR95357;

DT 16-DEC-1996 (first entry)

XX Residues 83-100 of myelin basic protein.

DE Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;  
 XX CD4+; T-cell; autoimmune disease; demyelination; central nervous system;  
 XX CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;  
 XX relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;  
 XX diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;  
 XX psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;  
 XX myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.

OS Synthetic.

FN WO9612737-A2.

PD 02-MAY-1996.

PF 25-OCT-1995; 95WO-US013682.

PR 25-OCT-1994; 94US-00328224.

PR 15-MAR-1995; 95US-00404228.

XX (IMVU-) IMMULOGIC PHARM CORP.

PI Smilek D, Samson M, Geffter M, Hsu D, Shi J, Paliard X, Devaux B;  
 PI Rothbard J, Franzen H;

XX WPI; 1996-230552/23.

XX Myelin basic derived peptide(s) and analogs - used in the treatment of  
 XX Multiple Sclerosis, psoriasis, Graves Disease, etc.

XX Claim 8; Fig 14; 91pp; English.

XX AAR95334-R95374 represent peptides derived from myelin basic protein  
 CC (MBP). Immunisation with MBP can be used to induce experimental allergic  
 CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+ T-  
 CC cell mediated autoimmune disease which results in demyelination of the  
 CC central nervous system, resulting in paralysis and other neurological  
 CC abnormalities. EAE is a commonly used animal model for human multiple  
 CC sclerosis (MS). These sequences can be used in compositions for treating  
 CC MS in a mammal. The composition acts to down regulate the autoimmune  
 CC response, and may be administered in an amount sufficient to prevent the  
 CC onset of symptoms of MS. The compositions may also be used to treat  
 CC advanced stage MS, especially relapsing-remitting MS, chronic progressive  
 CC MS or benign MS. These peptides may also be used in the treatment of  
 CC other diseases involving myelin autoantigens, including diabetes, Graves  
 CC disease, myasthenia gravis, Good Pasture's syndrome, psoriasis,  
 CC thyroiditis, and rheumatoid arthritis. Peptides derived from other myelin  
 CC autoantigens, such as myelin oligodendrocyte protein (MOG), proteolipid  
 CC protein (PLP), and myelin associated glycoprotein (MAG) can be used as  
 CC alternatives to these MBP peptides in these compositions

XX Sequence 18 AA;

Query Match 100.0%; Score 94; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ENPVVHFFKNIVTPRTP 17  
 |||||  
 DB 1 ENPVVHFFKNIVTPRTP 17

## RESULT 13

AAW73600  
 ID AAW73600 standard; peptide; 18 AA.

AC AAW73600;

DT 18-MAR-1999 (first entry)

DE Human myelin basic protein fragment.

XX Myelin basic protein; MBP; human; immunodominant region; inhibitor;  
KW immunosuppressant agent; multiple sclerosis; T cell proliferation;  
KV suppressor inducer.  
XX  
OS Homo sapiens.  
XX  
PN US5858960-A.  
XX  
PD 12-JAN-1999.  
XX  
PF 06-JUN-1995; 95US-00468540.  
XX  
PR 30-MAR-1990; 90US-00502559.  
PR 28-FEB-1992; 92US-00843752.  
PR 09-APR-1992; 92US-00865318.  
PR 09-APR-1993; 93US-00046354.  
XX  
PA (AUTO-) AUTOIMMUNE INC.  
XX  
PI Miller A, Weiner HL, Hafler DA, Al-Sabbagh A;  
XX  
DR MPI; 1999-119958/10.  
XX  
PT New peptides from immunodominant regions of human myelin basic protein -  
XX useful as immunosuppressants for treatment of multiple sclerosis.  
PS  
SQ Claim 1, Col 37; 32pp; English.  
XX  
CC This sequence represents a fragment of the human myelin basic protein  
CC (MBP). The peptides are immunodominant regions of MBP, and are used as  
CC the immunosuppressant agents of the invention. The peptides act on the  
CC response to MBP (or tissues containing it), specifically for treatment of  
CC multiple sclerosis (MS). They either induce energy in MBP-reactive T  
CC cells or actively suppress these cells by inhibiting their proliferation,  
CC possibly by inducing suppressor T cells. The peptides may also be used to  
CC detect specific T cells. The MBP fragments do not induce 'global  
CC immunosuppression upon prolonged use (increasing the risk of a patient  
CC developing certain malignancies), will not down regulate normal immune  
CC responses to pathogenic micro-organisms and are less toxic than drugs  
CC currently used for the treatment of MS, such as azathioprine (Imuran),  
CC and cyclosporin A  
XX  
SQ Sequence 18 AA;  
XX  
Query Match 100.0%; Score 94; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
XX  
RESULT 14  
AAV65533  
ID AAV65533 standard; peptide; 18 AA.  
XX  
AC AAV65533;  
XX  
DT 21-MAR-2000 (first entry)  
XX  
DE Myelin basic protein fragment MBP(85-102).  
XX  
KW Myelin basic protein; MBP; autoimmune mediated demyelinating disease;  
KW multiple sclerosis; encephalomyelitis; immune response; human.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO957241-A2.  
XX  
PD 11-NOV-1999.

XX  
PF 05-MAY-1999; 99WO-US009930.  
XX  
PR 05-MAY-1998; 98US-00073109.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Arim111 S, Deshpande S;  
XX  
DR MPI; 2000-072228/06.  
XX  
PT Novel peptides for treating autoimmune diseases of central nervous system  
XX characterized by demyelination.  
XX  
PS Example 1; Fig 1A; 57pp; English.  
XX  
CC The invention provides novel peptides derived from human myelin basic  
CC protein having an amino acid sequence Phe-X-Lys-Asn-Ile-Val-X-X-X-Thr-X-  
CC X, where X is any amino acid. The MBP peptides are used in the treatment  
CC of autoimmune mediated demyelinating disease like multiple sclerosis or  
CC the murine demyelinating experimental autoimmune encephalomyelitis. The  
CC therapeutic compositions comprising novel MBP peptides are used for  
CC inducing oral tolerance or general tolerance. The compositions are used  
CC to downregulate or eliminate autoreactive components of the immune system  
CC and treat autoreactive demyelinating, T-cell mediated immune response.  
CC The novel MBP peptides when administered into a subject are useful for  
CC inhibiting a T-cell mediated immune response against MBP, to treat the T-  
CC cell mediated immune response which causes a pathological condition of  
CC the nervous system e.g., multiple sclerosis. Prevention or suppression of  
CC MHC-restricted immune responses is done without any undesirable side  
CC effects, such as non-specific suppression of an individual's overall  
CC immune response. The MBP peptides provide a safer and more effective  
CC treatment by selectively suppressing autoimmune responses at the helper  
CC CD4+ T-cell levels. Sequences AAV6531-553 represent MBP peptides  
XX  
SQ Sequence 18 AA;  
XX  
Query Match 100.0%; Score 94; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
XX  
RESULT 15  
AAR32295  
ID AAR32295 standard; protein; 19 AA.  
XX  
AC AAR32295;  
XX  
DT 25-MAR-2003 (revised)  
DT 31-MAY-1993 (first entry)  
XX  
DE Sequence of synthetic peptide MBP 84-102 which corresp. to AAs 84-102 of  
XX myelin basic protein.  
XX  
KW Cytotoxin T lymphocyte response; epitope; antigen.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9301831-A1.  
XX  
PD 04-FEB-1993.  
XX  
PF 24-JUL-1992; 92WO-US006193.  
XX  
PR 25-JUL-1991; 91US-00735069.  
XX  
PA (IDEC-) IDEC PHARM CORP.  
XX  
PI Raychaudhuri S, Rastetter WH;



XX WPI; 1993-058526/07.  
XX  
XX New compsn. comprising an antigen and a formulation - to induce a  
PT cytotoxic T-lymphocyte response, useful for treating malaria, HIV,  
PT influenza, hepatitis, herpes, cancer, etc.  
XX  
XX  
XX Disclousure; Page 19; 56pp; English.  
PS  
CC Carbone and Bevan demonstrated that cytotoxic T-lymphocyte (CTL) induced  
CC in C57BL/6 mice by EG7-ova transfectant, and by cytoplasmically ova-  
CC loaded splenocytes recognise E14 cells coated with the peptide ova 258-  
CC 276. To determine whether soluble ovalbumin in AF induces similar CTL  
CC responses, spleen cells were prepared from immunised mice and stimulated  
CC in vitro with EG7-ova. The effectors were tested against E14 cells coated  
CC with the peptide ova 253-276 or with a control peptide derived from  
CC myelin basic protein (MBP 84-102). The results demonstrate that ova-AF  
CC primed CTL with a similar specificity to those primed by transfectants,  
CC or by cytoplasmically loaded ova. (Updated on 25-MAR-2003 to correct FN  
CC field.)  
XX  
SQ Sequence 19 AA;

Query Match 100.0%; Score 94; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.9e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRPP 17  
| | | | | | | | | | | | | | | | | | |  
DB 2 ENPVVHFFKNIVTPRPP 18

Search completed: June 7, 2005, 08:56:41  
Job time : 10.6321 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 7, 2005, 08:49:07 ; Search time 2.37824 Seconds  
(without alignments)  
533.603 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94

Sequence: 1 ENPVVHFFKNITVPRTP 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA:\*

- 1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/prodata/1/1aa/Backfillseq1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	100.0	17	3 US-09-137-759-3	Sequence 3, Appl1
2	94	100.0	17	3 US-09-378-244-3	Sequence 3, Appl1
3	94	100.0	18	2 US-08-468-540B-18	Sequence 18, Appl1
4	94	100.0	19	2 US-08-640-344-2	Sequence 2, Appl1
5	94	100.0	19	2 US-08-468-540B-9	Sequence 9, Appl1
6	94	100.0	19	2 US-08-468-540B-17	Sequence 17, Appl1
7	94	100.0	19	2 US-08-468-540B-24	Sequence 24, Appl1
8	94	100.0	19	3 US-08-297-395-1	Sequence 1, Appl1
9	94	100.0	19	3 US-09-024-220-2	Sequence 2, Appl1
10	94	100.0	19	3 US-08-960-190A-32	Sequence 32, Appl1
11	94	100.0	19	3 US-08-449-728-2	Sequence 2, Appl1
12	94	100.0	19	4 US-09-077-028A-15	Sequence 15, Appl1
13	94	100.0	19	4 US-09-740-003-2	Sequence 2, Appl1
14	94	100.0	20	2 US-08-640-344-1	Sequence 1, Appl1
15	94	100.0	20	2 US-08-640-344-3	Sequence 3, Appl1
16	94	100.0	20	2 US-08-640-344-4	Sequence 4, Appl1
17	94	100.0	20	2 US-08-640-344-5	Sequence 5, Appl1
18	94	100.0	20	2 US-08-640-344-6	Sequence 6, Appl1
19	94	100.0	20	2 US-08-640-344-7	Sequence 7, Appl1
20	94	100.0	20	3 US-08-960-190A-28	Sequence 28, Appl1
21	94	100.0	23	1 US-08-787-547-1	Sequence 1, Appl1
22	94	100.0	23	2 US-08-480-190-46	Sequence 46, Appl1
23	94	100.0	24	2 US-08-488-379-46	Sequence 46, Appl1
24	94	100.0	24	4 US-08-475-399A-46	Sequence 46, Appl1
25	94	100.0	24	4 US-09-339-043D-2501	Sequence 2501, Ap
26	94	100.0	24	4 US-08-077-255A-46	Sequence 46, Appl1
27	94	100.0	24	5 PCT-US93-07545-46	Sequence 46, Appl1

28	94	100.0	40	3 US-08-297-395-2	Sequence 2, Appl1
29	94	100.0	168	6 5194425-4	Patent No. 5194425
30	94	100.0	168	6 5194425-4	Patent No. 5194425
31	94	100.0	170	1 US-08-227-372-1	Sequence 1, Appl1
32	94	100.0	170	2 US-08-327-357A-1	Sequence 1, Appl1
33	94	100.0	170	3 US-08-470-397-1	Sequence 1, Appl1
34	94	100.0	170	3 US-09-007-520-1	Sequence 1, Appl1
35	94	100.0	170	3 US-08-462-351-3	Sequence 1, Appl1
36	94	100.0	170	3 US-09-055-263-1	Sequence 1, Appl1
37	94	100.0	170	3 US-09-007-520-1	Sequence 1, Appl1
38	94	100.0	170	4 US-08-342-408B-2	Sequence 2, Appl1
39	94	100.0	170	4 US-09-602-807-3	Sequence 3, Appl1
40	94	100.0	170	6 5194425-3	Patent No. 5194425
41	94	100.0	170	6 5194425-3	Patent No. 5194425
42	94	100.0	171	2 US-08-781-122-2	Sequence 2, Appl1
43	94	100.0	171	3 US-09-137-759-2	Sequence 2, Appl1
44	94	100.0	171	3 US-08-953-937-2	Sequence 2, Appl1
45	94	100.0	171	3 US-09-378-244-2	Sequence 2, Appl1

## ALIGNMENTS

```
RESULT 1
US-09-137-759-3
; Sequence 3, Application US/09137759
; Patent No. 6251396
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophil
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; FILE REFERENCE: 690068, 405C1
; CURRENT APPLICATION NUMBER: US/09/137,759
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
US-09-137-759-3
Query Match          100.0%; Score 94; DB 3; Length 17;
Best local Similarity 100.0%; Pred. No. 6.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 ENPVVHFFKNITVPRTP 17
Db       1 ENPVVHFFKNITVPRTP 17
RESULT 2
US-09-378-244-3
; Sequence 3, Application US/09378244
; Patent No. 6379670
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophil
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; FILE REFERENCE: 690068, 405C2
; CURRENT APPLICATION NUMBER: US/09/378,244
; CURRENT FILING DATE: 1999-08-19
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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
US-09-378-244-3

Query Match      100.0%; Score 94; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENPVVHFFKNIVTPRTP 17
Db      1 ENPVVHFFKNIVTPRTP 17

RESULT 3
US-08-468-540B-18
; Sequence 18, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafler, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,540B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5858980e
US-08-468-540B-18

Query Match      100.0%; Score 94; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENPVVHFFKNIVTPRTP 17
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Db      1 ENPVVHFFKNIVTPRTP 17

RESULT 4
US-08-640-344-2
; Sequence 2, Application US/08640344
; Patent No. 5824315
; GENERAL INFORMATION:
; APPLICANT: NAG, BISHWAJIT
; APPLICANT: MUKU, PRABHA
; APPLICANT: DESHPANDE, SHRIKANT
; TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC
; TITLE OF INVENTION: PEPTIDES FOR MHC MOLECULES
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,344
; FILING DATE: 30-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STORELLA ESQ., JOHN R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 14058-004800
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-640-344-2

Query Match      100.0%; Score 94; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.2e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENPVVHFFKNIVTPRTP 17
Db      2 ENPVVHFFKNIVTPRTP 18

RESULT 5
US-08-468-540B-9
; Sequence 9, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafler, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
```

COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,540B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jacobs, Seth H  
REGISTRATION NUMBER: 32,140  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: NO. 5858980E  
US-08-468-540B-9

Query Match 100.0%; Score 94; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
|||  
DB 2 ENPVVHFFKNIVTPRTP 18

RESULT 6  
US-08-468-540B-17  
Sequence 17, Application US/08468540B  
Patent No. 5858980  
GENERAL INFORMATION:  
APPLICANT: Weiner, Howard  
APPLICANT: Hafner, David  
APPLICANT: Miller, Ariel  
APPLICANT: Al-Sabbagh, Ahmad  
TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Darby & Darby P.C.  
STREET: 805 Third Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,540B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jacobs, Seth H

REGISTRATION NUMBER: 32,140  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: NO. 5858980E  
US-08-468-540B-17

Query Match 100.0%; Score 94; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
|||  
DB 2 ENPVVHFFKNIVTPRTP 18

RESULT 7  
US-08-468-540B-24  
Sequence 24, Application US/08468540B  
Patent No. 5858980  
GENERAL INFORMATION:  
APPLICANT: Weiner, Howard  
APPLICANT: Hafner, David  
APPLICANT: Miller, Ariel  
APPLICANT: Al-Sabbagh, Ahmad  
TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Darby & Darby P.C.  
STREET: 805 Third Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,540B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jacobs, Seth H  
REGISTRATION NUMBER: 32,140  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: NO. 5858980E  
US-08-468-540B-24

Query Match 100.0%; Score 94; DB 2; Length 19;

Beat Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
Db 2 ENPVVHFFKNIVTPRTP 18

## RESULT 8

US-08-297-395-1  
Sequence 1, Application US/08297395A  
Patent No. 6039947

## GENERAL INFORMATION:

APPLICANT: Howard L. Weiner  
APPLICANT: David A. Hafler  
TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT  
FILE REFERENCE: 1010/05723US  
CURRENT APPLICATION NUMBER: US/08/297,395A  
CURRENT FILING DATE: 1994-08-11  
EARLIER APPLICATION NUMBER: 08/059,189  
EARLIER FILING DATE: 1993-05-06  
EARLIER APPLICATION NUMBER: 07/502,559  
EARLIER FILING DATE: 1990-03-30  
EARLIER APPLICATION NUMBER: PCT/US88/02139  
EARLIER FILING DATE: 1988-06-24  
EARLIER APPLICATION NUMBER: 07/065,734  
EARLIER FILING DATE: 1987-06-24  
NUMBER OF SEQ ID NOS: 84  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-297-395-1

Query Match 100.0%; Score 94; DB 3; Length 19;  
Beat Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
Db 2 ENPVVHFFKNIVTPRTP 18

## RESULT 9

US-09-024-220-2  
Sequence 2, Application US/09024220  
Patent No. 6197311

## GENERAL INFORMATION:

APPLICANT: RAYCHAUDHURI, Syamal  
BLACK, Amelia  
RASTETTER, William H.  
TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE  
RESPONSES

## NUMBER OF SEQUENCES: 2

## CORRESPONDENCE ADDRESS:

ADDRESS: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

APPLICATION NUMBER: US/09/024,220

FILING DATE: 17-Feb-1998

CLASSIFICATION: <Unknown>

24-JUL-1992

25-JUL-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476,674

FILING DATE: <Unknown>

APPLICATION NUMBER: US 07/919,787

FILING DATE: 24-JUL-1992

APPLICATION NUMBER: US 07/735,069

FILING DATE: 25-JUL-1991

ATTORNEY/AGENT INFORMATION:

NAME: Teekin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-149

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 100.0%; Score 94; DB 3; Length 19;  
Beat Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
Db 2 ENPVVHFFKNIVTPRTP 18

## RESULT 10

US-08-960-190A-32

Sequence 32, Application US/08960190A

Patent No. 6232445

## GENERAL INFORMATION:

APPLICANT: Rhode, Peter R.  
APPLICANT: Acevedo, Jorge  
APPLICANT: Burkhardt, Martin  
APPLICANT: Jiao, Jin-an  
APPLICANT: Wong, Hing C.  
TITLE OF INVENTION: SOLUBLE H2G COMPLEXES AND  
TITLE OF INVENTION: METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: usa  
ZIP: 02109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/960,190A

FILING DATE: 29-OCT-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Cortes, Peter F

REGISTRATION NUMBER: 33,860

REFERENCE/DOCKET NUMBER: 48002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

TELEX:  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-960-190A-32

Query Match 100.0%; Score 94; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17  
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 11  
US-08-449-728-2  
; Sequence 2, Application US/08449728  
; Patent No. 6270769  
; GENERAL INFORMATION:  
; APPLICANT: STAMAL RAYCHAUDHURI  
; APPLICANT: WILLIAM H. RASTETTER  
; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC  
; TITLE OF INVENTION: T-LYMPHOCYTE RESPONSES  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM PS/2 Model 502 or 555X  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: Wordperfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,728  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/735,069  
; FILING DATE: 25-JUL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 194/160  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-449-728-2

Query Match 100.0%; Score 94; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ENPVVHFFKNIVTPRTP 17  
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 12  
US-09-077-028A-15  
; Sequence 15, Application US/09077028A  
; Patent No. 6531133  
; GENERAL INFORMATION:  
; APPLICANT: HAVA LOREBERGOM-GALSKI  
; APPLICANT: IDA STEINBERGER  
; APPLICANT: EVELINE BERAUD  
; APPLICANT: IRINA MARIANOVSKY  
; APPLICANT: SHAI YARKONI  
; TITLE OF INVENTION: PSEUDOMONAS EXOTOXIN-MYELIN BASIC PROTEIN CHIMERIC  
; FILE REFERENCE: LOREBERGOM-1  
; CURRENT APPLICATION NUMBER: US/09/077,028A  
; CURRENT FILING DATE: 1998-05-18  
; PRIOR FILING DATE: 1995-11-17  
; PRIOR FILING DATE: 1995-11-17  
; PRIOR FILING DATE: 1995-12-26  
; PRIOR APPLICATION NUMBER: IL116559  
; PRIOR FILING DATE: 1995-12-26  
; PRIOR APPLICATION NUMBER: PCT/IL96/00151  
; PRIOR FILING DATE: 1996-11-17  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-077-028A-15

Query Match 100.0%; Score 94; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17  
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 13  
US-09-740-003-2  
; Sequence 2, Application US/09740003  
; Patent No. 6733763  
; GENERAL INFORMATION:  
; APPLICANT: RAYCHAUDHURI, SYAMAL  
; APPLICANT: RASTETTER, WILLIAM H.  
; APPLICANT: BLACK, AMELIA  
; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES  
; FILE REFERENCE: 37003/275802  
; CURRENT APPLICATION NUMBER: US/09/740,003  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 09/024,220  
; PRIOR FILING DATE: 1998-02-17  
; PRIOR APPLICATION NUMBER: 08/476,674  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/351,001  
; PRIOR FILING DATE: 1994-12-07  
; PRIOR APPLICATION NUMBER: 08/919,787  
; PRIOR FILING DATE: 1997-08-29  
; PRIOR APPLICATION NUMBER: 07/735,069  
; PRIOR FILING DATE: 1991-07-25  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-740-003-2

Query Match 100.0%; Score 94; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 09:33:36 ; Search time 38 Seconds  
(without alignments)  
43.044 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94

Sequence: 1 ENPVVHFFKNIVTPRTP 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2991

Minimum DB seq length: 0  
Maximum DB seq length: 17

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	45.7	14	2	S12904
2	24	25.5	11	2	A54348
3	24	25.5	16	2	S03405
4	24	25.5	16	2	A59046
5	23	24.5	9	2	S55696
6	23	24.5	14	2	PH1628
7	23	24.5	16	2	S65520
8	22	23.4	10	2	A58365
9	22	23.4	7	2	S42820
10	21	22.3	15	2	S62641
11	20	21.3	10	2	A43977
12	20	21.3	13	2	PH1620
13	20	21.3	13	2	PC2369
14	20	21.3	14	2	S62374
15	20	21.3	15	2	A35417
16	20	21.3	16	2	A49255
17	20	21.3	16	2	PH1640
18	20	21.3	16	2	S09084
19	19.5	20.7	9	2	PT0080
20	19	20.2	12	2	PQ0730
21	19	20.2	13	2	PH1593
22	19	20.2	13	2	A61514
23	19	20.2	15	2	B61457
24	19	20.2	15	2	G60977
25	19	20.2	15	2	S59492
26	19	20.2	15	2	PA0093
27	19	20.2	16	2	A28144
28	19	20.2	16	2	A46236
29	19	20.2	16	2	S42237

30	19	20.2	16	2	B48406	annexin VI homolog
31	19	20.2	17	2	S32587	L-ascorbate peroxi
32	18	19.1	8	2	B39745	endoglycosylcerami
33	18	19.1	11	4	C61497	seed protein ws-18
34	18	19.1	11	4	PC2390	trichotozin I - fu
35	18	19.1	11	4	PC2392	trichotozin III -
36	18	19.1	12	2	B39690	neural cell adhesi
37	18	19.1	13	1	UNBO	neurotensin - bovi
38	18	19.1	13	2	A33208	calreticulin, hepa
39	18	19.1	13	2	A40207	cell surface glyco
40	18	19.1	14	2	S29632	xylian 1,4-beta-xy
41	18	19.1	14	2	S59495	formate dehydrogen
42	18	19.1	14	2	A60158	disaggregatase - M
43	18	19.1	14	2	B56884	Pax-QNR, long form
44	18	19.1	15	2	B33208	calreticulin, uter
45	18	19.1	15	2	S27248	pseudogermin - whe

## ALIGNMENTS

RESULT 1  
S12904  
protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)  
C:Species: Pisaster ochraceus  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S12904  
R:Sanhara, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.  
FEBS Lett. 273, 223-226, 1990  
A>Title: Identification of the sites in myelin basic protein that are phosphorylated by n  
A:Reference number: S12904; WUID:91032186; PMID:1699809  
A:Accession: S12904  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <SN>  
A:Cross-references: UNIPROT:Q7M3W4  
C:Keywords: phosphotransferase

Query Match  
Best Local Similarity 100.0%; Pred. No. 0.41;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NIVTPRTP 17  
DB 1 NIVTPRTP 8

RESULT 2  
A54348  
N-acetylglucosamine-6-sulfatase (EC 3.1.6.14) - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996  
C:Accession: A54348  
R:Shilatifard, A.; Cummings, R.D.  
Biochemistry 33, 4273-4282, 1994  
A>Title: Purification and characterization of N-acetylglucosamine-6-sulfatase frc  
A:Reference number: A54348; WUID:94206936; PMID:8155645  
A:Accession: A54348  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <SHI>  
C:Keywords: sulfuric ester hydrolase

Query Match  
Best Local Similarity 62.5%; Pred. No. 5.5e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 FPNIVTP 14  
DB 4 FPNIVTP 11

RESULT 3

S03405  
hydrogenase (EC 1.18.99.1) small chain - Alcaligenes eutrophus (fragment)  
C:Species: Alcaligenes eutrophus  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 13-Sep-1998  
C:Accession: S03405  
R:Lorenz, B.; Schneider, K.; Kretzin, H.; Schlegel, H.G.  
Biochim. Biophys. Acta 995, 1-9, 1989  
A:Title: Immunological comparison of subunits isolated from various hydrogenases of aerc  
A:Reference number: S03404; PMID:89166625; PMID:2493816  
A:Accession: S03405  
A:Molecule type: protein  
A:Residues: 1-16 <LOR>  
A:Experimental source: strain H16, DMS 541  
C:Superfamily: hydrogenase (NiFe), small chain  
C:Keywords: hydrogen metabolism; iron-sulfur protein; membrane bound; metalloprotein; ni

Query Match  
Best Local Similarity 25.5%; Score 24; DB 2; Length 16;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PRTP 17  
|||  
Db 5 PRTP 8

RESULT 4  
A59046  
alpha-conotoxin MII - cone shell (Conus magus)  
C:Species: Conus magus (magus cone)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: A59046  
R:Cartier, G.E.; Yoshikami, D.; Gray, W.R.; Luo, S.; Olivera, B.M.; McIntosh, J.M.  
J. Biol. Chem. 271, 7522-7528, 1996  
A:Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine recept  
A:Reference number: A59046; PMID:96205934; PMID:8631783  
A:Accession: A59046  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-16 <CAR>  
A:Cross-references: UNIPROT:P56636  
C:Superfamily: alpha-conotoxin  
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro  
F:1-16/Product: alpha-conotoxin MII #status experimental <MAT>  
F:2-8,3-16/Diulfide Bonds: #status experimental  
F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match  
Best Local Similarity 25.5%; Score 24; DB 2; Length 16;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPVH 6  
|||  
Db 5 NPVH 9

RESULT 5  
S55696  
phosphoenolpyruvate carboxykinase - Trypanosoma brucei  
C:Species: Trypanosoma brucei  
C:Date: 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S55696  
R:Hunt, M.; Koehler, P.  
Biochim. Biophys. Acta 1249, 15-22, 1995  
A:Title: Purification and characterization of phosphoenolpyruvate carboxykinase from Try  
A:Reference number: S55696; PMID:95284106; PMID:7766679  
A:Accession: S55696  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <HUN>  
A:Cross-references: UNIPROT:Q7M355

Query Match  
Best Local Similarity 24.5%; Score 23; DB 2; Length 9;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 4; Conservative 3; Mismatches 0; Indels 2; Gaps 1;  
QY 3 PVHFFKNI 11  
|::|::|  
Db 2 PITH--KNL 8

RESULT 6  
PH1628  
Ig H chain V-D-J region (clone B-Jess 151) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1628  
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-Jess mice  
A:Reference number: PH1580; PMID:93301609; PMID:8315387  
A:Accession: PH1628  
A:Molecule type: DNA  
A:Residues: 1-14 <LBV>  
A:Experimental source: bone marrow pre-B lymphocyte  
C:Keywords: immunoglobulin

Query Match  
Best Local Similarity 24.5%; Score 23; DB 2; Length 14;  
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 HFFKNIV 12  
|::|::|  
Db 4 HYNSML 10

RESULT 7  
S65520  
phospholipase A2 (EC 3.1.1.4) - Malayan spitting cobra (fragment)  
N:Contains: muscarinic acetylcholine receptor inhibitor  
C:Species: Naja naja sputatrix (Malayan spitting cobra)  
C:Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 09-Jul-2004  
C:Accession: S65520  
R:Miyouhi, S.; Tu, A.T.  
Arch. Biochem. Biophys. 328, 17-25, 1996  
A:Title: Phospholipase A2) from Naja naja sputatrix venom is a muscarinic acetylcholine  
A:Reference number: S65520; PMID:96195757; PMID:8638927  
A:Accession: S65520  
A:Molecule type: protein  
A:Residues: 1-16 <MIY>  
A:Cross-references: UNIPROT:Q10756  
C:Superfamily: phospholipase A2  
C:Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; presy

Query Match  
Best Local Similarity 24.5%; Score 23; DB 2; Length 16;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 8 FKNIVTPRT 17  
|::|::|  
Db 5 FKNIVQCTVP 14

RESULT 8  
A58365  
neuropeptide FRRamide - blue mussel  
N:Alternate names: FRRamide-related decapeptide; Mytilus FRRamide  
C:Species: Mytilus edulis (blue mussel)  
C:Date: 20-Nov-1996 #sequence\_revision 22-Nov-1996 #text\_change 09-Jul-2004  
C:Accession: A58365  
R:Fujisawa, Y.; Ikeda, T.; Nomoto, K.; Yasuda-Kamatani, Y.; Minakata, H.; Kenny, P.T.M.;  
Comp. Biochem. Physiol. C 102, 91-95, 1992  
A:Title: The FRRamide-related decapeptide of Mytilus contains a D-amino acid residue.  
A:Reference number: A58365; PMID:93047882; PMID:1358533  
A:Accession: A58365  
A:Molecule type: protein.  
A:Residues: 1-10 <FUJ>

A:Cross-references: UNIPROT:P42560  
A:Experimental source: anterior byssus retractor muscle  
C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide  
F:2/Modified site: D-leucine (Leu) #status experimental  
F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 23.4%; Score 22; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 HFFK 9  
|||  
Db 6 HFFK 9

## RESULT 9

S42620  
aggrecan - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)

C:Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 24-Jul-1998  
C:Accession: S42620

R:Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.  
Matrix Biol. 14, 171-179, 1994

A:Title: Aggrecan in bovine tendon.

A:Reference number: S42620; PMID:7520336

A:Accession: S42620

A:Molecule type: protein

A:Residues: 1-7 <VOG>

A:Experimental source: flexor tendon

C:Keywords: cartilage

Query Match 22.3%; Score 21; DB 2; Length 7;  
Best Local Similarity 80.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 11 IYTPR 15  
|||  
Db 3 IVSPR 7

## RESULT 10

S62641  
porphobilinogen synthase (EC 4.2.1.24) - green alga (Scenedesmus obliquus) (fragment)

N:Alternate names: 5-aminolevulinic acid dehydratase

C:Species: Scenedesmus obliquus

C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C:Accession: S62641

R:Stolz, M.; Doernemann, D.

Eur. J. Biochem. 236, 600-608, 1996

A:Title: Purification, metal cofactor, N-terminal sequence and subunit composition of a

A:Reference number: S62641; PMID:9615670; PMID:8612634

A:Accession: S62641

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <STO>

A:Cross-references: UNIPROT:O9S8B1

C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 22.3%; Score 21; DB 2; Length 15;  
Best Local Similarity 80.0%; Pred. No. 2.6e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 11 IYTPR 15  
|||  
Db 11 IVSPR 15

## RESULT 11

A43977

FMRFamide-like protein - tobacco hornworm

C:Species: Manduca sexta (tobacco hornworm)

C:Date: 11-Feb-1993 #sequence\_revision 11-Feb-1993 #text\_change 09-Jul-2004

C:Accession: A43977

R:Kingan, T.G.; Teplow, D.B.; Phillips, J.M.; Riehm, J.P.; Rao, K.R.; Hildebrand, J.G.;  
Peptides 11, 849-856, 1990

A:Title: A new peptide in the FMRFamide family isolated from the CNS of the hawkmoth, Mar

A:Reference number: A43977; PMID:91045350; PMID:2235684

A:Accession: A43977

A:Molecule type: protein

A:Residues: 1-10 <KIN>

A:Cross-references: UNIPROT:P18523

C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 21.3%; Score 20; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 2.4e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 VVHFF 8  
|||  
Db 3 VVHSP 7

## RESULT 12

PH1620

Ig H chain V-D-J region (clone B-1ess 40) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C:Accession: PH1620

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-1ess mice

A:Reference number: PH1580; PMID:93301609; PMID:8315387

A:Accession: PH1620

A:Molecule type: DNA

A:Residues: 1-13 <LEU>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 21.3%; Score 20; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 IYTP 14  
|||  
Db 6 IYTP 9

## RESULT 13

PC2369  
unidentified 85k protein [imported] - Bacillus cereus (strain ts-4) (fragment)

C:Species: Bacillus cereus

C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004

C:Accession: PC2369

R:Matsumoto, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.

BioSci. Biotechnol. Biochem. 59, 231-235, 1995

A:Title: Identification of DNA-binding proteins changed after induction of sporulation in

A:Reference number: PC2369; PMID:95218265; PMID:776022

A:Accession: PC2369

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <MAS>

A:Cross-references: UNIPROT:Q7M0L4

Query Match 21.3%; Score 20; DB 2; Length 13;  
Best Local Similarity 57.1%; Pred. No. 3.2e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ENPVVHF 7  
|||  
Db 7 ENPVMAKF 13

## RESULT 14

S62374

alpha-1-antichymotrypsin - human (fragment)

```

c/species: Homo sapiens (man)
c/date: 24-Aug-1996 #sequence revision 13-Mar-1997 #text change 09-Jul-2004

```

C;Accession: S62374

R; Tsuda, M.; Sei, Y.; Ohkubo, T.; Yamamura, M.; Kamiguchi, H.; Akatsuka, A.; Tsuda, T.; Eur. J. Biochem. 235 821-827 1996

A;Title: The defective secretion of a naturally occurring alpha-1-antichymotrypsin vari

A:Reference number: S62374; MUID:96184564; PMID:8654434

A:Status: preliminary: not compared with conceptual translation

A:Molecule type: mRNA

A;Residues: 1-14 <TSU>  
A;Cross-references: INTBPT.09MT19, INTBPT.095DW8, INTBPT.09N177

U/C/OBBSBBTCTEACED: UNFNOY:QONCJ; UNFNOY:QOCDNB; UNFNOY:QONT//

Query Match	Score	DB	Length
21.3%	20	2	14

Best Local Similarity	18.2%	Pred. NO.	3.5e+03;						
Matches	2:	Conservative	3:	Mismatches	6:	Indels	0:	Gaps	0:

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QY 5 VHEFKNI VTPR 15

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Db      : | : | :
        2 IFMSKVTPNK 12
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## RESULT 15

A35417

28K serine proteinase homolog - bovine (fragment)  
C\_Snoctas: Bos taurus (cartil)

C:\species: *Drosophila melanogaster* (cellar)  
C:\Date: 18-Jan-1991 #sequence revision 18-Jan-1991 #text change 09-Jul-2004

C/Accession: A35417

R;HO, F.L.; Carpenter, M.K.; Smille, L.B.; Gambardini, A.G.  
Biochem. Biophys. Res. Commun. 170, 769-774, 1990

A/Title: Co-purification of proteases with basic fibroblast growth factor (FGF).

A/Reference number: A35417; MUID:90343797; PMID:2200404  
 2/Accession: A35417

A/Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <HQA>  
A;Cross-references: INITPROT:07M3G3

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Query Match	21.34	Score 20;	DB 2;	Length 15;
Post Local Client	66.78	Prod No	3 89.03	

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Best local similarity 88.7%; Freq. NO. 3.0e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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# Index

QY 9 KNIVIP 14

Db 10 KGYTP 15 .

Search completed: June 7, 2005, 09:37:15

Job time : 40 secs



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RA Chaganti R.S.K., Koppers R., Dalla-Favera R.;
RT "Hypermutation of multiple proto-oncogenes in B-cell diffuse large-
RL cell lymphomas.";
RN Nature 412:341-346(2001).
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=966234102; PubMed=8650231; DOI=10.1073/pnas.93.12.6129;
RA Buslinger M., Kilx N., Pfeiffer P., Graninger P.G., Kozmik Z.;
RT "Deregulation of PAX-5 by translocation of the Emu enhancer of the Igh
RL locus adjacent to two alternative PAX-5 promoters in a diffuse large-
RT cell lymphoma.";
RN Proc. Natl. Acad. Sci. U.S.A. 93:6129-6134(1996).
DR EMBL; AF268279; AAK25737.1; -.
DR EMBL; AF386790; AAK70869.1; -.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1809 MW; 3F95BB53FB3F7A8E CRC64;

Query Match
Best Local Similarity 31.9%; Score 30; DB 2; Length 15;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 KNIVTPRT 16
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DB 5 KNVPTPT 12

RESULT 3
O6LCH6 PRELIMINARY; PRT; 15 AA.
AC O6LCH6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE B-cell specific transcription factor (Fragment).
GN Name=PAX-5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RX MEDLINE=966234102; PubMed=8650231; DOI=10.1073/pnas.93.12.6129;
RA Buslinger M., Kilx N., Pfeiffer P., Graninger P.G., Kozmik Z.;
RT "Deregulation of PAX-5 by translocation of the Emu enhancer of the Igh
RL locus adjacent to two alternative PAX-5 promoters in a diffuse large-
RT cell lymphoma.";
RN Proc. Natl. Acad. Sci. U.S.A. 93:6129-6134(1996).
DR EMBL; U56837; AAB16834.1; -.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1835 MW; 3F95ABE3FB3F7A8E CRC64;

Query Match
Best Local Similarity 31.9%; Score 30; DB 2; Length 15;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 KNIVTPRT 16
   |||||
   |||||
DB 5 KNVPTPT 12

RESULT 4
O8VNS8 PRELIMINARY; PRT; 16 AA.
AC O8VNS8;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE Cdc6 protein (Fragment).
GN Name=Cdc6;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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OC Enterobacteriaceae; Escherichia.
OK NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=413/89-1;
RA Benkel P., Chakraborty T.;
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277443; CAC81838.1; -.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1826 MW; 0D5EA97E0C676A12 CRC64;

Query Match
Best Local Similarity 29.8%; Score 28; DB 2; Length 16;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTP 14
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DB 2 QQPVVVVGEMLVTP 15

RESULT 5
O69142 PRELIMINARY; PRT; 15 AA.
AC O69142;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Protein SIC (Fragment).
GN Name=sic;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OK NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AP1;
RX MEDLINE=98298075; PubMed=9632622;
RA Berge A., Rasmussen M., Bjorck L.;
RT "Identification of an insertion sequence located in a region encoding
RT virulence factors of Streptococcus pyogenes.";
DR EMBL; AF064540; AAC38769.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1552 MW; 87655FEF047401FF CRC64;

Query Match
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Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 KNIVTPPT 17
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DB 4 KPSTVPTPT 12

RESULT 6
Q7RSN9 PRELIMINARY; PRT; 10 AA.
AC Q7RSN9;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=PY00316;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OK NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguioni S.V., Suh B.B., Koof T.W., Perrea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
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RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldlyum T.V.,  
RA Cho J.K., Quackenbush J., Sedegh M., Shoib A., Cummings L.M.,  
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,  
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdey A.B.,  
RA van Lin L.H., Jans C.J., Waters A.P., Smith H.O., White O.R.,  
RA Salberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,  
RA Carucci D.J.,  
RT "Genome sequence and comparative analysis of the model rodent malaria  
RT parasite Plasmodium yoelii yoelii.";  
RL Nature 419:512-519 (2002).  
CC -! CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC EMBL; AABL0100088; EAA22681.1; -.  
DR Hypothetical protein.  
KW NON TER  
SQ SEQUENCE 10 AA; 1209 MW; 3F8986573B42C047 CRC64;  
  
Query Match 26.6%; Score 25; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 3e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 NPVHFFKNI 11  
DB 2 NPVHFFKNI 8  
  
RESULT 7  
Q9BY9 PRELIMINARY; PRT; 12 AA.  
AC Q9BY9;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Amyloid beta protein (Fragment).  
CN Name:APP;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCB1\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21082082; PubMed=11214319; DOI=10.1038/35054550;  
RX Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
RA O'Brien S.J.;  
RT "Molecular phylogenetics and the origins of placental mammals.";  
RL Nature 409:614-618 (2001).  
DR EMBL; AY011354; AAG47389.1; -.  
FT NON TER  
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;  
  
Query Match 26.6%; Score 25; DB 2; Length 12;  
Best Local Similarity 40.0%; Pred. No. 3.7e+03;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2 NPVHFFKNI 11  
DB 1 NPTVKKFEQ 10  
  
RESULT 8  
Q6JC79 PRELIMINARY; PRT; 12 AA.  
AC Q6JC79;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE APP (Fragment).  
OS Solenodon paradoxus (Hispaniolan solenodon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Insectivora; Solenodontidae; Solenodon.  
OX NCB1\_TaxID=9805;  
RN [1]

RP SEQUENCE FROM N.A.  
RX PubMed=15190349; DOI=10.1038/nature02597;  
RX Roca A.L., Bar-Gal G.K., Elzirik E., Helgen K.M., Maria R.,  
RA Springer M.S., O'Brien S.J., Murphy W.J.;  
RT "Mesozoic origin for West Indian insectivores.";  
RL Nature 429:649-651 (2004).  
DR EMBL; AY530068; AAS67633.1; -.  
FT NON TER  
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;  
  
Query Match 26.6%; Score 25; DB 2; Length 12;  
Best Local Similarity 40.0%; Pred. No. 3.7e+03;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2 NPVHFFKNI 11  
DB 1 NPTVKKFEQ 10  
  
RESULT 9  
Q71B00 PRELIMINARY; PRT; 12 AA.  
AC Q71B00;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE APP (Fragment).  
OS Cynocephalus volans (Philippine flying lemur).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Dermoptera; Cynocephalidae; Cynocephalus.  
OX NCB1\_TaxID=110931;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX Elzirik E., Murphy W.J., Springer M.S., O'Brien S.J.;  
RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF535039; AAQ10584.1; -.  
FT NON TER  
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;  
  
Query Match 26.6%; Score 25; DB 2; Length 12;  
Best Local Similarity 40.0%; Pred. No. 3.7e+03;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2 NPVHFFKNI 11  
DB 1 NPTVKKFEQ 10  
  
RESULT 10  
Q71B01 PRELIMINARY; PRT; 12 AA.  
AC Q71B01;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE APP (Fragment).  
OS Urogale everetti.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Urogale.  
OX NCB1\_TaxID=192726;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX Elzirik E., Murphy W.J., Springer M.S., O'Brien S.J.;  
RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF535038; AAQ10583.1; -.  
FT NON TER  
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;  
  
Query Match 26.6%; Score 25; DB 2; Length 12;  
Best Local Similarity 40.0%; Pred. No. 3.7e+03;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2 NPVHFFKNI 11

```
Db 1 NPTYKFFEQM 10

RESULT 11
Q9BFR4 PRELIMINARY; PRT; 12 AA.
AC Q9BFR4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Amyloid beta protein (Fragment).
GN Name=APP;
OS Manus pentadactyla.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Pholidota; Manidae; Manis.
RN NCBI_TaxID=143292;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319; DOI=10.1038/35054550;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
DR Nature 409:614-618(2001).
FT EMBL; AY011374; AAG47409.1; -.
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;

Query Match 26.6%; Score 25; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPVHFFPKNI 11
ID Q9BFR5 PRELIMINARY; PRT; 12 AA.
AC Q9BFR5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Amyloid beta protein (Fragment).
GN Name=APP;
OS Ursus arctos (Brown bear) (Grizzly bear).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
RN NCBI_TaxID=9644;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319; DOI=10.1038/35054550;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
DR Nature 409:614-618(2001).
FT EMBL; AY011373; AAG47408.1; -.
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;

Query Match 26.6%; Score 25; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPVHFFPKNI 11
ID Q9BFR6 PRELIMINARY; PRT; 12 AA.
```

```
AC Q9BFR6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Amyloid beta protein (Fragment).
GN Name=APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN NCBI_TaxID=9615;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319; DOI=10.1038/35054550;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
DR Nature 409:614-618(2001).
FT EMBL; AY011372; AAG47407.1; -.
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;

Query Match 26.6%; Score 25; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPVHFFPKNI 11
ID Q9BFR7 PRELIMINARY; PRT; 12 AA.
AC Q9BFR7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Amyloid beta protein (Fragment).
GN Name=APP;
OS Panthera onca (Jaguar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Panthera.
RN NCBI_TaxID=9690;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319; DOI=10.1038/35054550;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
DR Nature 409:614-618(2001).
FT EMBL; AY011371; AAG47406.1; -.
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;

Query Match 26.6%; Score 25; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPVHFFPKNI 11
ID Q9BFR8 PRELIMINARY; PRT; 12 AA.
AC Q9BFR8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Amyloid beta protein (Fragment).
GN Name=APP;
OS Leopardus pardalis (Ocelot).
```



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.  
OX NCB1\_TaxID=32538;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21082082; PubMed=11214319; DOI=10.1038/35054550;  
RA O'Brien S.J.;  
RA Murphy W.J.; Bizirik E.; Johnson W.E.; Zhang Y.P.; Ryder O.A.;  
RT "Molecular phylogenetics and the origins of placental mammals.";  
RL Nature 409:614-618(2001).  
DR EMBL; AY011370; AAC47405.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;  
QY 2 NPVHFFKNI 11  
|||:  
1 NPTYKFFEQM 10

Search completed: June 7, 2005, 09:36:30  
UOD time : 166 secs

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## OM protein - protein search, using sw model

Run on: June 7, 2005, 09:33:36 ; Search time 67 Seconds  
(without alignments)  
98.133 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94

Sequence: 1 ENPVVHFKNIVTPRTP 17

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 664154

Minimum DB seq length: 0  
Maximum DB seq length: 17Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1908:\*
- 2: geneseqp1908:\*
- 3: geneseqp2000:\*
- 4: geneseqp2001:\*
- 5: geneseqp2002:\*
- 6: geneseqp2003:\*
- 7: geneseqp2003:\*
- 8: geneseqp2004:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	100.0	17	3	AAy69395
2	94	100.0	17	5	AAO20308
3	94	100.0	17	5	AAE26359
4	94	100.0	17	5	AAE23935
5	94	100.0	17	6	ABP97941
6	94	100.0	17	6	ABR56063
7	94	100.0	17	6	AAO19672
8	94	100.0	17	7	ADSE0773
9	94	100.0	17	8	ADK67704
10	94	100.0	17	8	ADL18291
11	89	94.7	17	2	AAK44116
12	89	94.7	17	2	AAK95360
13	89	94.7	17	2	AAW73601
14	89	94.7	17	3	AAy66534
15	89	94.7	17	3	AAK44118
16	87	92.6	17	2	AAK95354
17	87	92.6	17	2	AAW72353
18	87	92.6	17	2	AAW73602
19	83	88.3	16	2	AAK44117
20	83	88.3	16	2	AAK95361
21	83	88.3	16	3	AAy66535
22	83	88.3	16	5	AAE23936
23	82	87.2	15	2	AAK44120
24	82	87.2	15	2	AAW05498
25	82	87.2	15	2	AAW04856

26	82	87.2	15	2	AAW78826	AAW78826 Myelin ba
27	82	87.2	15	2	AAW73599	AAW73599 Human mye
28	82	87.2	15	3	AAy85545	AAy85545 Human MBP
29	82	87.2	15	3	AAy85528	AAy85528 Human MBP
30	82	87.2	15	3	AAK33638	AAK33638 MHC class
31	82	87.2	15	3	AAK12630	AAK12630 Human mye
32	82	87.2	15	4	AAK99039	AAK99039 Vaccine r
33	82	87.2	15	4	AAK93734	AAK93734 Human mye
34	82	87.2	15	5	AAO20312	AAO20312 Myelin ba
35	82	87.2	15	5	AAO17039	AAO17039 Myelin ba
36	82	87.2	15	5	ABP52207	ABP52207 Myelin ba
37	82	87.2	15	5	ABR84358	ABR84358 Human BPI
38	82	87.2	15	6	AAE33459	AAE33459 MBP85-99
39	82	87.2	15	6	ABR44413	ABR44413 Human bas
40	82	87.2	15	6	ABR44414	ABR44414 Human bas
41	82	87.2	15	6	ABU96590	ABU96590 MHC class
42	82	87.2	15	7	ADH89023	ADH89023 Ordered p
43	82	87.2	15	7	ADC06708	ADC06708 MBP p85-9
44	82	87.2	15	7	ADK38272	ADK38272 Immunomod
45	82	87.2	15	8	ADL29030	ADL29030 MBP (85-9

## ALIGNMENTS

RESULT 1	
AAy69395	
ID	AAy69395 standard; peptide; 17 AA.
XX	
XX	AAy69395;
DT	19-JUN-2000 (first entry)
XX	
DE	Peptide derived from a human myelin basic protein.
XX	
XX	Human; myelin basic protein; oligodendroglial cell; Th2 immune response;
KW	Th2-type cytokine; analogue; multiple sclerosis.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	WO200011027-A1.
XX	
PD	02-MAR-2000.
XX	
PP	19-AUG-1999; 99WO-US019033.
XX	
PR	20-AUG-1998; 98US-00137759.
XX	
PA	(NOVS ) NOVARTIS AG.
PA	(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA	(NEUR-) NEUROCRINE BIOSCIENCES INC.
PI	Gaur A, Conlon P, Ling NC, Staehlin T, Crowe P;
DR	WPI; 2000-224661/19.
XX	
PT	Inducing a Th2 immune response and a persistent systemic immune response
PT	to myelin basic protein, MBP, or a peptide analog of MBP for use in
PT	treating multiple sclerosis, by administering compositions comprising
PT	peptide analogs of MBP.
XX	
PS	Example 10; Fig 8; 112pp; English.
XX	
CC	The present sequence represents a peptide derived from human myelin basic
CC	protein. Myelin basic protein is found in the cytoplasm of human
CC	oligodendroglial cells. Peptide analogue derived from the present
CC	sequence are administered to a patient in need to induce a Th2 immune
CC	response (i.e. production of T cells producing one or more Th2-type
CC	cytokines) and/or a persistent systemic immune response to myelin basic
CC	protein. These peptide analogues are at least seven amino acids long,
CC	derived from residues 83-99 of human myelin basic protein and altered
CC	from the native sequence at least at positions 91, 95 or 97. The peptide

CC analogs are especially useful in the treatment of multiple sclerosis  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
RESULT 2  
AAO20308  
ID AAO20308 standard; peptide; 17 AA.  
AC AAO20308;  
XX  
DT 31-MAY-2002 (first entry)  
XX  
DE Myelin basic protein (MBP) epitope peptide region 83-99.  
XX  
KM MBP; myelin basic protein; epitope; antiasthmatic; tolerogenic peptide;  
XX dermatological; anti-allergic; neuroprotective; antithyroid; antianemic;  
XX vasotropic; antiinflammatory; immunosuppressive; antidiabetic; class I;  
XX major histocompatibility complex; MHC; class II; autoimmune thyroiditis;  
XX hypersensitivity disorder; antigen; allergy; extrinsic asthma; urticaria;  
XX autoimmune haemolytic anaemia; atopic dermatitis; allergic rhinitis;  
XX autoimmune disease; multiple sclerosis; Grave's disease; sarcoidosis;  
XX systemic sclerosis; polymyositis; diabetes; transplant rejection;  
XX antiviral CD8+.  
XX  
OS Unidentified.  
XX  
PN WO200216410-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-GB003702.  
XX  
PR 21-AUG-2000; 2000GB-00020618.  
XX  
PR 14-JUN-2001; 2001GB-00014547.  
XX  
XX (UYBR-) UNITV BRISTOL.  
XX  
PI Wraith DC, Anderson SM, Maza G, Ponsford M, Streeter HB;  
XX  
XX MPI; 2002-292056/33.  
XX  
DR Selecting tolerogenic peptide useful for treating autoimmune diseases  
XX e.g. multiple sclerosis, involves selecting peptide which binds major  
XX histocompatibility complex class I or II molecule without further  
XX processing.  
XX  
PS Claim 12; Page 28; 55pp; English.  
XX  
XX The invention relates to a method for selecting a tolerogenic peptide,  
XX comprising selecting a peptide which is capable of binding to a major  
XX histocompatibility complex (MHC) class I or II molecule without further  
XX processing. The peptides of the invention are useful for preventing a  
XX disease such as hypersensitivity disorder, and also for treating and/or  
XX preventing a disease in a subject. The method involves identifying an  
XX antigen for the disease, identifying an epitope (antigen processing  
XX independent epitope) for the antigen, and administering the epitope to  
XX the subject. The peptides of the invention are also useful for treating  
XX allergies such as extrinsic asthma, atopic dermatitis, allergic rhinitis,  
XX urticaria, autoimmune diseases such as multiple sclerosis, autoimmune  
XX thyroiditis, Grave's disease, systemic sclerosis, sarcoidosis, autoimmune  
XX haemolytic anaemia, polymyositis, diabetes, etc., and transplant  
XX rejection. The peptides are also useful for modifying antiviral CD8+  
XX responses in a tolerogenic fashion. This sequence represents an epitope  
XX of the invention of peptide region 83-99 of Myelin basic protein (MBP)

XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
RESULT 3  
AAE26359  
ID AAE26359 standard; peptide; 17 AA.  
AC AAE26359;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Peptide related to myelin basic protein.  
XX  
KM Th2 immune response; myelin basic protein; MBP; vaccine; MS;  
XX multiple sclerosis; antisclerotic.  
XX  
OS Unidentified.  
XX  
XX US6379670-B1.  
XX  
PN 30-APR-2002.  
XX  
PD 19-AUG-1999; 99US-00378244.  
XX  
PF 18-NOV-1994; 94US-00342408.  
XX  
PR 20-AUG-1998; 98US-00137759.  
XX  
XX (NEUR-) NEUROCRINE BIOSCIENCES INC.  
XX  
PA (NOVS) NOVARTIS AG.  
XX  
PI Gaur A, Conlon P, Ling NC, Staehelin T, Crowe PD;  
XX  
XX MPI; 2002-461895/49.  
XX  
DR Inducing Th2 immune responses to Myelin Basic Protein (MBP) by  
XX PT administering the MBP peptide analog CGP 77116, useful for treating  
XX PT Multiple Sclerosis.  
XX  
PS Disclosure; Col 35-36; 49pp; English.  
XX  
XX The present invention relates to a novel method for inducing Th2 immune  
XX responses to Myelin Basic Protein (MBP) or a peptide analogue of MBP in a  
XX patient. The method involves administering a composition comprising the  
XX MBP peptide analogue CGP 77116 (NBI-5788). The method is useful for  
XX treating multiple sclerosis (MS). Sequences of the invention are also  
XX used as vaccines. The present sequence is a peptide related to human MBP  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
RESULT 4  
AAE23935  
ID AAE23935 standard; peptide; 17 AA.  
XX  
AC AAE23935;  
XX

DT 10-SEP-2002 (first entry)  
XX Peptide analogue used in the invention.  
DE Autoimmune disease; multiple sclerosis; MS; Jbeta; Cbeta; Vbeta; Dbeta;  
KW immunosuppressive; T-cell receptor; therapy.  
XX Unidentified.  
OS  
XX WO200216434-A1.  
PN 28-FEB-2002.  
XX  
XX 22-AUG-2000; 2000WO-US022988.  
PF 22-AUG-2000; 2000WO-US022988.  
PR (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX Zhang JZ;  
PI WPI; 2002-454317/48.  
XX A novel peptide used in the treatment of autoimmune disease e.g. multiple  
PT sclerosis.  
PS Example 2; Fig 2; 64pp; English.  
SQ  
CC The invention relates to a peptide used in the treatment of autoimmune  
CC disease e.g. multiple sclerosis (MS). More particularly, it concerns a T-  
CC cell receptor sequence found in some MS patients and methods for its  
CC detection. T cell receptors comprise alpha and beta chains, with beta  
CC chains comprising the following regions from N-terminus to C-terminus:  
CC Vbeta-Jbeta-Cbeta. T cell receptors naturally vary in the Vbeta-  
CC Jbeta-Cbeta region. The peptides of the invention are used for treating  
CC autoimmune disease e.g. multiple sclerosis. The present sequence is a  
CC peptide analogue used in the exemplification of the invention  
CC  
SQ Sequence 17 AA:  
Query Match 100.0%; Score 94; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
Db 1 ENPVVHFFKNIVTPRTP 17  
RESULT 5  
ABP97941  
ID ABP97941 standard; peptide; 17 AA.  
XX  
AC ABP97941;  
XX  
XX 17-JUN-2003 (first entry)  
DT  
XX Amino acid sequence of a glycopeptide.  
DE Glycopeptide; serum; immunosorption column; antibody;  
KW multiple sclerosis.  
XX  
XX Synthetic.  
OS  
XX Key Location/Qualifiers  
FH Modified-site 1 /note= "H attached"  
FT Modified-site 2 /note= "glycosylated residue"  
PT Modified-site 17 /note= "OH attached"  
XX  
XX WO2003009887-A2.

XX 06-FEB-2003.  
PD 25-JUL-2002; 2002WO-EP008274.  
XX 25-JUL-2001; 2001IT-FI000144.  
PF 25-JUL-2001; 2001IT-FI000144.  
PR (UYFI-) UNIV FIRENZE.  
XX Pinto F, Papini AM, Chelli M, Rovero P, Lolli F;  
XX WPI; 2003-312632/30.  
XX  
XX Immunosorption column, useful for treating multiple sclerosis, contains  
PT glycopeptides able to react with disease-specific autoantibodies.  
XX  
XX Claim 4; Page 6; 13pp; English.  
PS ABP97937-44 represent glycopeptides of a formula given in the  
CC specification. The glycopeptides are used to produce columns of the  
CC invention. The specification describes immunosorption columns,  
CC containing conjugates comprising glycopeptides which are able to  
CC recognize antibodies implicated in multiple sclerosis. The column removes  
CC harmful antibodies selectively, leaving all other components of the serum  
CC unchanged. The column is used to treat multiple sclerosis  
CC  
SQ Sequence 17 AA:  
Query Match 100.0%; Score 94; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
Db 1 ENPVVHFFKNIVTPRTP 17  
RESULT 6  
ABR56063  
ID ABR56063 standard; peptide; 17 AA.  
XX  
AC ABR56063;  
XX  
DT 06-AUG-2003 (first entry)  
XX  
DE Glycopeptide #5 for diagnosis and treatment of multiple sclerosis.  
KW Glycopeptide; neuroprotective; autoantibody; multiple sclerosis.  
XX  
XX Synthetic.  
OS  
XX Key Location/Qualifiers  
FH Modified-site 2 /note= "Asn(Glc)"  
FT  
PN WO2003000733-A2.  
XX  
XX 03-JAN-2003.  
PD  
XX 19-JUN-2002; 2002WO-EP006767.  
XX  
XX 22-JUN-2001; 2001IT-FI000114.  
PR (UYFI-) UNIV FIRENZE.  
XX Papiini AM, Chelli M, Rovero P, Lolli F;  
XX WPI; 2003-354383/33.  
XX  
XX Novel glycopeptides comprising a specific tetrapeptide, useful as  
PT diagnostic tools for identifying multiple sclerosis.  
XX  
XX Claim 7; Page 12; 14pp; English.  
PS

XX The present invention relates to glycopeptides (ABR56059-ABR56066). The  
CC glycopeptides have high specificity in recognizing autoantibodies  
CC involved in multiple sclerosis pathology, and thus are effectively used  
CC in diagnosis and treatment for multiple sclerosis  
XX  
SQ Sequence 17 AA:  
Query Match 100.0%; Score 94; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6,1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
1 |||||  
Db 1 ENPVVHFFKNIVTPRTP 17  
RESULT 7  
AA019672  
ID AAO19672 standard; peptide; 17 AA.  
XX  
AC AAO19672;  
XX  
DT 28-MAR-2003 (first entry)  
XX  
DE Human myelin basic protein MBP minimal epitope.  
XX  
KW Human; Ig; immunoglobulin; immunotherapy; immune disease; MBP;  
KW Fcpepsilon receptor; autoimmune disease; constant region; heavy chain;  
KW antihistaminic; antiallergic; antiinflammatory; dermatological; G22;  
KW antichratic; antineumatic; antidiabetic; neuroprotective;  
KW myelin basic protein; minimal epitope.  
XX  
OS Homo sapiens.  
XX  
PN WO200288317-A2.  
XX  
PD 07-NOV-2002.  
XX  
PF 01-MAY-2002; 2002WO-US013527.  
XX  
PR 01-MAY-2001; 2001US-00847208.  
PR 24-OCT-2001; 2001US-00000439.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
PI Saxon A, Zhang K, Zhu D;  
XX  
PT MPI; 2003-103456/09.  
XX  
DR  
XX  
PT New fusion molecules comprising polypeptide sequences that bind to IgG  
PT inhibitory receptor and native IgE receptor, useful for treating IgE-  
PT mediated hypersensitivity reactions, e.g. asthma or allergies, or  
PT autoimmune diseases.  
XX  
PS Claim 23; Page 116; 116pp; English.  
XX  
XX The present invention relates to a fusion molecule comprising a first  
CC polypeptide sequence capable of specific binding to a native IgG  
CC inhibitory receptor consisting of an immune receptor tyrosine-based  
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
CC functionally connected to a second polypeptide sequence capable of  
CC specific binding directly or indirectly to a native IgE receptor  
CC (Fcpepsilon). Also provided are nucleotide sequences encoding such a  
CC fusion protein. The fusion molecules and compositions are useful for  
CC treating an IGE-mediated biological response, preferably an IGE-mediated  
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
CC anaphylactic shock; or autoimmune diseases such as Rheumatoid arthritis,  
CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,  
CC or symptoms resulting from, a type I hypersensitivity reaction in a  
CC subject receiving immunotherapy. The present sequence is the human myelin  
CC basic protein minimal epitope which can be used in a fusion protein of

CC the invention  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6,1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
1 |||||  
Db 1 ENPVVHFFKNIVTPRTP 17  
RESULT 8  
ADE50773  
ID ADE50773 standard; peptide; 17 AA.  
XX  
AC ADE50773;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Wild-type human myelin basic protein peptide analog.  
XX  
KW Human; Th2; immune response; myelin basic protein; peptide analog;  
KW proteolysis; multiple sclerosis; neuroprotective; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2002176866-A1.  
XX  
PD 28-NOV-2002.  
XX  
PF 20-MAR-2002; 2002US-00104973.  
XX  
PR 18-NOV-1994; 94US-00342408.  
PR 20-AUG-1998; 98US-00137759.  
PR 19-AUG-1999; 99US-00378244.  
XX  
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
PI Gaur A, Conlon P, Ling NC, Staehelin T, Crowe PD;  
XX  
PT MPI; 2003-615722/58.  
XX  
DR  
XX  
PT Inducing a Th2 immune response to myelin basic protein or its peptide  
PT analog in a patient, useful for treating multiple sclerosis, comprises  
PT administering an amount of a pharmaceutical composition comprising a  
PT peptide analog.  
XX  
PS Disclosure; SEQ ID NO 3; 52pp; English.  
XX  
XX The invention discloses a method for inducing a Th2 immune response to  
CC myelin basic protein or its peptide analog in a patient, comprising  
CC administering a composition comprising a peptide analog in combination  
CC with a carrier/adjuvant or diluent. The peptide analog comprises at least  
CC 7 amino acids selected from residues 83 to 99 of human myelin basic  
CC protein, where: the L-lysine at position 91, L-arginine at position 97 or  
CC L-threonine at position 95, is altered to another amino acid, and one to  
CC three L-amino acids selected from valine at position 86 or 87, histidine  
CC at position 88, threonine at position 95 or 98, and proline at position  
CC 99 are altered to an amino acid other than the amino acid present in the  
CC native protein at that position or the L-lysine at position 91 is altered  
CC to another amino acid and the N- and/or C-terminal amino acid are altered  
CC to another amino acid, such that upon administration of the peptide  
CC analog in vivo proteolysis is reduced. The peptide analog comprises 7-17  
CC amino acids and one to four additional altered residues. The N-terminal  
CC amino acid is residue 83 of human myelin basic protein. At least one of  
CC the additional L-amino acids selected from residues 83 to 90 and 92 to 99  
CC is substituted with a charged amino acid. The method is useful for  
CC treating multiple sclerosis using peptide analogs of human myelin basic  
CC protein. The sequence presented is the wild-type human myelin basic  
CC protein peptide analog.  
XX

TYPE: PRT  
ORGANISM: synthetic construct  
US-09-836-433-30

Query Match 100.0%; Score 94; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
Db 3 ENPVVHFFKNIVTPRTP 19

## RESULT 13

US-09-859-012-35  
Sequence 35, Application US/09859012  
Publication No. US20040253632A1  
GENERAL INFORMATION:  
APPLICANT: RHODE, PETER  
APPLICANT: WITTMAN, VAUGHAN  
APPLICANT: WEIDMANZ, JON A.  
APPLICANT: BURKHARDT, MARTIN  
APPLICANT: CARD, KIMBERLYN F.  
APPLICANT: TAL, RONY  
APPLICANT: ACEVEDO, JORGE  
APPLICANT: WONG, HING C.  
TITLE OF INVENTION: MODULATION OF T CELL RECEPTOR INTERACTIONS  
FILE REFERENCE: 49444 (71758)  
CURRENT APPLICATION NUMBER: US/09/859,012  
CURRENT FILING DATE: 2001-05-16  
PRIOR APPLICATION NUMBER: 60/206,920  
PRIOR FILING DATE: 2000-05-25  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 35  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-859-012-35

Query Match 100.0%; Score 94; DB 11; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
Db 3 ENPVVHFFKNIVTPRTP 19

## RESULT 14

US-09-859-012-49  
Sequence 49, Application US/09859012  
Publication No. US20040253632A1  
GENERAL INFORMATION:  
APPLICANT: RHODE, PETER  
APPLICANT: WITTMAN, VAUGHAN  
APPLICANT: WEIDMANZ, JON A.  
APPLICANT: BURKHARDT, MARTIN  
APPLICANT: CARD, KIMBERLYN F.  
APPLICANT: TAL, RONY  
APPLICANT: ACEVEDO, JORGE  
APPLICANT: WONG, HING C.  
TITLE OF INVENTION: MODULATION OF T CELL RECEPTOR INTERACTIONS  
FILE REFERENCE: 49444 (71758)  
CURRENT APPLICATION NUMBER: US/09/859,012  
CURRENT FILING DATE: 2001-05-16  
PRIOR APPLICATION NUMBER: 60/206,920  
PRIOR FILING DATE: 2000-05-25  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 49  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-859-012-49

Query Match 100.0%; Score 94; DB 11; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
Db 3 ENPVVHFFKNIVTPRTP 19

## RESULT 15

US-10-081-281-33  
Sequence 33, Application US/10081281  
Publication No. US20020151707A1  
GENERAL INFORMATION:  
APPLICANT: Kindsvogel, Wayne  
Gross, Jane A.  
Sheppard, Paul  
TITLE OF INVENTION: Immune Mediators and Related Methods  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/081,281  
FILING DATE: 20-Feb-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/261,811A  
FILING DATE: 03-Mar-1999  
APPLICATION NUMBER: US 08/480,002  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/482,133  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/483,241  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 60/005,964  
FILING DATE: 27-OCT-1995  
APPLICATION NUMBER: US 08/657,581  
FILING DATE: 07-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Parent, Annette S.  
REGISTRATION NUMBER: 014058-005630US  
REFERENCE/DOCKET NUMBER: 014058-005630US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-10-081-281-33  
Query Match 100.0%; Score 94; DB 13; Length 21;  
Best Local Similarity 100.0%; Pred. No. 5.8e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHHFFKNIVTPRPP 17  
Db 2 ENPVVHHFFKNIVTPRPP 18

Search completed: June 7, 2005, 09:25:08  
Job time : 8.45769 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 09:33:36 ; Search time 40 Seconds  
(without alignments)  
31.726 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94

Sequence: 1 ENPVVHFFKNIVTPRTP 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 177072

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

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2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*

3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*

4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*

5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/prodata/1/1aa/Backfilltest.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	100.0	17	3	US-09-137-759-3
2	94	100.0	17	3	US-09-378-244-3
3	89	94.7	17	2	US-08-468-540B-19
4	87	92.6	17	2	US-08-468-540B-20
5	82	87.2	15	1	US-08-787-547-37
6	82	87.2	15	2	US-08-468-540B-16
7	82	87.2	15	2	US-08-400-796-16
8	82	87.2	15	4	US-09-606-254-11
9	82	87.2	16	2	US-08-468-540B-21
10	77	81.9	14	2	US-08-468-540B-23
11	77	81.9	15	2	US-08-468-540B-22
12	76	80.9	14	3	US-08-342-408B-3
13	76	80.9	16	4	US-09-009-953-3
14	75	79.8	17	3	US-09-137-759-6
15	75	79.8	17	3	US-09-378-244-6
16	72	76.6	13	2	US-08-540-388-4
17	72	76.6	13	2	US-08-735-253-19
18	71	75.5	17	3	US-09-137-759-7
19	71	75.5	17	3	US-09-378-244-7
20	70	74.5	14	1	US-08-787-547-36
21	69	73.4	17	3	US-09-137-759-8
22	69	73.4	17	3	US-09-378-244-8
23	68	72.3	13	1	US-08-787-547-38
24	68	72.3	13	5	PCT-US94-10257A-22
25	68	72.3	13	5	PCT-US94-10257A-24
26	66	70.2	17	3	US-09-137-759-5
27	66	70.2	17	3	US-09-378-244-5

28	64	68.1	17	3	US-09-137-759-4	Sequence 4, Appl1
29	64	68.1	17	3	US-09-378-244-4	Sequence 4, Appl1
30	60	63.8	12	4	US-09-403-752A-126	Sequence 126, App
31	60	63.8	12	4	US-09-551-151A-126	Sequence 126, App
32	57	60.6	13	1	US-08-483-021-4	Sequence 9, Appl1
33	56	59.6	10	3	US-08-159-339A-1097	Sequence 1097, Ap
34	56	59.6	10	3	US-08-159-339A-1109	Sequence 1109, Ap
35	53	56.4	14	3	US-08-855-925A-6	Sequence 6, Appl1
36	52	55.3	10	4	US-09-606-254-9	Sequence 9, Appl1
37	48	51.1	12	3	US-08-462-351-9	Sequence 9, Appl1
38	48	51.1	12	4	US-09-602-807-9	Sequence 9, Appl1
39	34	36.2	15	2	US-08-400-796-11	Sequence 11, Appl1
40	33	35.1	9	2	US-08-340-283-13	Sequence 13, Appl1
41	30	31.9	10	3	US-08-159-339A-461	Sequence 461, App
42	30	31.9	14	3	US-09-313-677-3	Sequence 3, Appl1
43	30	31.9	16	4	US-08-077-797A-49	Sequence 49, Appl1
44	30	31.9	16	4	US-09-546-013-78	Sequence 78, Appl1
45	30	31.9	16	5	PCT-US94-01238-49	Sequence 49, Appl1

#### ALIGNMENTS

```

RESULT 1
; Sequence 3, Application US/09137759
; Patent No. 6251396
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophil
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN
; FILE REFERENCE: 690068.405C1
; CURRENT APPLICATION NUMBER: US/09137,759
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; US-09-137-759-3

Query Match      100.0%; Score 94; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENPVVHFFKNIVTPRTP 17
Db      1 ENPVVHFFKNIVTPRTP 17

RESULT 2
; Sequence 3, Application US/09378244
; Patent No. 6379670
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophil
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN
; FILE REFERENCE: 690068.405C2
; CURRENT APPLICATION NUMBER: US/09378,244
; CURRENT FILING DATE: 1999-08-19

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NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
OTHER INFORMATION: Synthesis  
US-09-378-244-3

Query Match 100.0%; Score 94; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.4e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRT 17  
1 ENPVVHFFKNIVTPRT 17

Db 1 ENPVVHFFKNIVTPRT 17

RESULT 3  
US-08-468-540B-19  
Sequence 19, Application US/08468540B  
Patent No. 5858980  
GENERAL INFORMATION:  
APPLICANT: Weiner, Howard  
APPLICANT: Hafley, David  
APPLICANT: Miller, Ariel  
APPLICANT: Al-Sabbagh, Ahmad  
TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby P.C.  
STREET: 805 Third Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,540B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jacobs, Seth H  
REGISTRATION NUMBER: 32,140  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: NO. 5858980e  
US-08-468-540B-19

Query Match 94.7%; Score 89; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.2e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NEPVHFFKNIVTPRT 17

Db 1 NEPVHFFKNIVTPRT 16

RESULT 4  
US-08-468-540B-20  
Sequence 20, Application US/08468540B  
Patent No. 5858980  
GENERAL INFORMATION:  
APPLICANT: Weiner, Howard  
APPLICANT: Hafley, David  
APPLICANT: Miller, Ariel  
APPLICANT: Al-Sabbagh, Ahmad  
TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby P.C.  
STREET: 805 Third Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,540B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jacobs, Seth H  
REGISTRATION NUMBER: 32,140  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: NO. 5858980e  
US-08-468-540B-20

Query Match 92.6%; Score 87; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.8e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRT 16  
2 ENPVVHFFKNIVTPRT 17

Db 2 ENPVVHFFKNIVTPRT 17

RESULT 5  
US-08-787-547-37  
Sequence 37, Application US/08787547  
Patent No. 5783567  
GENERAL INFORMATION:  
APPLICANT: Hedley, Mary Lynne  
APPLICANT: Curley, Joanne M.  
APPLICANT: Langer, Robert S.  
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY  
TITLE OF INVENTION: OF NUCLEIC ACID  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:

ADDRESSER: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/787,547  
FILING DATE: 22-JAN-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 08191/003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-787-547-37

Query Match 87.2%; Score 82; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. Se-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPR 15  
DB 1 ENPVVHFFKNIVTPR 15

RESULT 6  
US-08-468-540B-16  
Sequence 16, Application US/08468540B  
Patent No. 5858980  
GENERAL INFORMATION:  
APPLICANT: Weiner, Howard  
APPLICANT: Hafner, David  
APPLICANT: Miller, Ariel  
APPLICANT: Al-Sabbagh, Ahmad  
TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Darby & Darby P.C.  
STREET: 805 Third Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,540B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jacobs, Seth H  
REGISTRATION NUMBER: 32,140  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 5858980e  
US-08-468-540B-16

Query Match 87.2%; Score 82; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. Se-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPR 15  
DB 1 ENPVVHFFKNIVTPR 15

RESULT 7  
US-08-400-796-16  
Sequence 16, Application US/08400796  
Patent No. 5874531  
GENERAL INFORMATION:  
APPLICANT: STROMINGER, JACK L.  
APPLICANT: MICHERPENNIG, KAI  
TITLE OF INVENTION: IDENTIFICATION OF SELF AND NON-SELF  
TITLE OF INVENTION: ANTIGENS IMPLICATED IN AUTOIMMUNE DISEASE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSER: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/400,796  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: TWOMEY, MICHAEL J.  
REGISTRATION NUMBER: 38,349  
REFERENCE/DOCKET NUMBER: H0498/7015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
ORGANISM: HOMO SAPIENS  
US-08-400-796-16

Query Match 87.2%; Score 82; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 5e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPR 15  
| | | | | | | | | |  
Db 1 ENPVVHFFKNIVTPR 15

## RESULT 8

US-09-606-254-11  
; Sequence 11, Application US/09606254  
; Patent No. 6531130  
; GENERAL INFORMATION:  
; APPLICANT: Steinman, Lawrence  
; APPLICANT: Ruiz, Pedro  
; TITLE OF INVENTION: Treatment of Demyelinating Autoimmune  
; TITLE OF INVENTION: Disease with Ordered Peptides  
; FILE REFERENCE: STAN-129  
; CURRENT APPLICATION NUMBER: US/09/606,254  
; CURRENT FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/142,479  
; PRIOR FILING DATE: 1999-07-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 11  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-09-606-254-11

Query Match 87.2%; Score 82; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPR 15  
| | | | | | | | | |  
Db 1 ENPVVHFFKNIVTPR 15

## RESULT 9

US-08-468-540B-21  
; Sequence 21, Application US/08468540B  
; Patent No. 5858980  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, Howard  
; APPLICANT: Hafler, David  
; APPLICANT: Miller, Ariel  
; APPLICANT: Al-Sabbagh, Ahmad  
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby P.C.  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,540B  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:

NAME: Jacobs, Seth H  
REGISTRATION NUMBER: 32,140  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX:

INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 5858980e  
US-08-468-540B-21

Query Match 87.2%; Score 82; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPR 15  
| | | | | | | | | |  
Db 2 ENPVVHFFKNIVTPR 16

## RESULT 10

US-08-468-540B-23  
; Sequence 23, Application US/08468540B  
; Patent No. 5858980  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, Howard  
; APPLICANT: Hafler, David  
; APPLICANT: Miller, Ariel  
; APPLICANT: Al-Sabbagh, Ahmad  
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby P.C.  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,540B  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jacobs, Seth H  
; REGISTRATION NUMBER: 32,140  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-527-7700  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 5858980e  
US-08-468-540B-23

Query Match 81.9%; Score 77; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred.No.3.1e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2 NPVHFFKNIVTPR 15  
Db 1 NPVHFFKNIVTPR 14

RESULT 11  
US-08-468-540B-22  
; Sequence 22, Application US/08468540B  
; Patent No. 5858980  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, Howard  
; APPLICANT: Hatler, David  
; APPLICANT: Miller, Ariel  
; APPLICANT: Al-Sabbagh, Ahmad  
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby P.C.  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,540B  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jacobs, Seth H  
; REGISTRATION NUMBER: 32,140  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-527-7700  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: NO. 5858980e  
US-08-468-540B-22

Query Match 81.9%; Score 77; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred.No.3.3e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 ENPVHFFKNIVTP 14  
Db 2 ENPVHFFKNIVTP 15

RESULT 12  
US-08-342-408B-3  
; Sequence 3, Application US/08342408B  
; Patent No. 6328499  
; GENERAL INFORMATION:  
; APPLICANT: Ling, Nicholas  
; APPLICANT: Gaur, Amitabh

; APPLICANT: Conlon, Paul J.  
; APPLICANT: Seilman, Lawrence  
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE  
; TITLE OF INVENTION: SCLERODIS USING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/342,408B  
; FILING DATE: 18-NOV-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6329499tenburg, Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 690068.405  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-342-408B-3

Query Match 80.9%; Score 76; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred.No.4.5e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 4 VVHFFKNIVTPRP 17  
Db 1 VVHFFKNIVTPRP 14

RESULT 13  
US-09-009-953-3  
; Sequence 3, Application US/09009953  
; Patent No. 6413517  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; TITLE OF INVENTION: Identification of Broadly  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/009,953  
; FILING DATE: 21-Jan-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/036,713

FILING DATE: 23-JAN-1997  
APPLICATION NUMBER: US 60/037,432  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-011520US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-009-953-3

Query Match 80.9%; Score 76; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.2e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VVHFFKNIVTPRT 17  
|||  
DB 1 VVHFFKNIVTPRT 14

RESULT 14  
US-09-137-759-6  
; Sequence 6, Application US/09137759  
; Patent No. 6251396  
; GENERAL INFORMATION:  
; APPLICANT: Gaur, Amitabh  
; APPLICANT: Conlon, Paul J.  
; APPLICANT: Ling, Nicholas C.  
; APPLICANT: Staehlin, Theophil  
; APPLICANT: Crowe, Paul D.  
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING  
; FILE REFERENCE: 690068.405C1  
; CURRENT APPLICATION NUMBER: US/09137,759  
; CURRENT FILING DATE: 1998-08-20  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Where Xaa is a D-alanine residue  
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
US-09-137-759-6

Query Match 79.8%; Score 75; DB 3; Length 17;  
Best Local Similarity 87.5%; Pred. No. 8e-06;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPVHFAFNVTPRT 17  
|||  
DB 2 NPVHFAFNVTPRT 17

RESULT 15  
US-09-378-244-6  
; Sequence 6, Application US/09378244  
; Patent No. 6379670

GENERAL INFORMATION:  
; APPLICANT: Gaur, Amitabh  
; APPLICANT: Conlon, Paul J.  
; APPLICANT: Ling, Nicholas C.  
; APPLICANT: Staehlin, Theophil  
; APPLICANT: Crowe, Paul D.  
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING  
; FILE REFERENCE: 690068.405C2  
; CURRENT APPLICATION NUMBER: US/09378,244  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Where Xaa is a D-alanine residue  
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
; OTHER INFORMATION: Synthesis  
US-09-378-244-6

Query Match 79.8%; Score 75; DB 3; Length 17;  
Best Local Similarity 87.5%; Pred. No. 8e-06;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPVHFAFNVTPRT 17  
|||  
DB 2 NPVHFAFNVTPRT 17

Search completed: June 7, 2005, 09:39:12  
Job time : 41 secs



XX  
DR MPI: 1993-351657/44.  
XX

PT New peptide(s) derived from human myelin basic protein - used for  
PT suppressing auto-immune response, partic. in treating multiple sclerosis.  
XX

PS Claim 1; Page 29; 118pp; English.  
XX

CC The peptide represents residues 84-100 of human myelin basic protein  
CC (hMBP). The fragment comprises an immunodominant epitope of hMBP which  
CC was identified by overlapping 20-mer oligopeptide sequence analysis using  
CC T-cell line assays. The peptide can be used to stop proliferation of  
CC human T-cells specific for MBP or to elicit active suppression of such T-  
CC cells. They are also used partic. for the treatment of multiple  
CC sclerosis. The peptide is also useful for identifying CD4+ T-cells  
CC reactive with MBP. See also AAR44114-25. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX

SQ Sequence 17 AA;

Query Match 92.6%; Score 87; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.7e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ENPVVHFFKNIVTPRT 16  
|||  
Db 2 ENPVVHFFKNIVTPRT 17

Search completed: June 7, 2005, 09:38:28  
Job time : 70 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 08:38:56 ; Search time 8.63212 Seconds  
(without alignments)  
761.681 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94

Sequence: 1 ENPVVHFKNIVTPRT 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp19808:\*  
2: geneseqp19908:\*  
3: geneseqp20008:\*  
4: geneseqp20018:\*  
5: geneseqp20028:\*  
6: geneseqp20038:\*  
7: geneseqp20048:\*  
8: geneseqp20058:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	94	100.0	17 3 AAY69395	Aay69395 Peptide d
2	94	100.0	17 5 AAO20308	Aao20308 Myelin ba
3	94	100.0	17 5 AAE26359	Aae26359 Peptide r
4	94	100.0	17 5 AAE23935	Aae23935 Peptide a
5	94	100.0	17 6 ABP97941	Abp97941 Amino aci
6	94	100.0	17 6 ABR56063	AbR56063 Glycopept
7	94	100.0	17 6 AAO19672	Aao19672 Human mye
8	94	100.0	17 7 ADE50773	Ade50773 Wild-type
9	94	100.0	17 8 ADK67704	Adk67704 Human mye
10	94	100.0	17 8 ADL18291	Adl18291 Human mye
11	94	100.0	18 2 AAR44115	Aar44115 Human mye
12	94	100.0	18 2 AAR53557	Aar53557 Residues
13	94	100.0	18 2 AAW73600	Aaw73600 Human mye
14	94	100.0	18 3 AAY66533	Aay66533 Myelin ba
15	94	100.0	19 2 AAR32295	Aar32295 Sequence
16	94	100.0	19 2 AAR44114	Aar44114 Human mye
17	94	100.0	19 2 AAR44123	Aar44123 Human mye
18	94	100.0	19 2 AAR85132	Aar85132 Human MBP
19	94	100.0	19 2 AAW05719	Aaw05719 Residues
20	94	100.0	19 2 AAR93366	Aar93366 Residues
21	94	100.0	19 2 AAR93355	Aar93355 Residues
22	94	100.0	19 2 AAR93358	Aar93358 Residues
23	94	100.0	19 2 AAW34183	Aaw34183 Bc-MBP (84
24	94	100.0	19 2 AAW34180	Aaw34180 Residues
25	94	100.0	19 2 AAW18021	Aaw18021 Human BPP

26	94	100.0	19 2 AAW44071	Aaw44071 Human mye
27	94	100.0	19 2 AAW73607	Aaw73607 Human mye
28	94	100.0	19 2 AAW73616	Aaw73616 Human mye
29	94	100.0	19 3 AAY58992	Aay58992 Myelin ba
30	94	100.0	19 3 AAY85560	Aay85560 Human MBP
31	94	100.0	19 3 AAY85550	Aay85550 Human MBP
32	94	100.0	19 3 AAY66532	Aay66532 Myelin ba
33	94	100.0	19 3 AAY66543	Aay66543 Myelin ba
34	94	100.0	19 3 AAB12618	Aab12618 Human mye
35	94	100.0	19 3 AAB12613	Aab12613 Human mye
36	94	100.0	19 4 AAM99040	Aam99040 Vaccine r
37	94	100.0	19 4 AAB74440	Aab74440 Ovalbumin
38	94	100.0	19 4 AAG65171	Aag65171 Myelin ba
39	94	100.0	19 5 AAB31665	Abg31665 Myelin ba
40	94	100.0	20 2 AAR94618	Aar94618 Myelin ba
41	94	100.0	20 2 AAR95392	Aar95392 Residues
42	94	100.0	20 2 AAW34187	Aaw34187 Bc-MBP (83
43	94	100.0	20 2 AAW34188	Aaw34188 Bc-MBP (83
44	94	100.0	20 2 AAW34184	Aaw34184 Bc-MBP (83
45	94	100.0	20 2 AAW34185	Aaw34185 Bc-MBP (83

## ALIGNMENTS

RESULT 1  
AAY69395  
ID AAY69395 standard; peptide; 17 AA.  
XX  
AC AAY69395;  
XX  
DT 19-JUN-2000 (first entry)  
XX  
DE Peptide derived from a human myelin basic protein.  
XX  
KW Human; myelin basic protein; oligodendroglial cell; Th2 immune response;  
KW Th2-type cytokine; analogue; multiple sclerosis.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO200011027-A1.  
XX  
PD 02-MAR-2000.  
XX  
PP 19-AUG-1999; 99WO-US019033.  
XX  
PR 20-AUG-1998; 98US-00137759.  
XX  
XX (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-BRENDINGEN VERB GES MBH.  
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
XX  
PI Gaur A, Conlon P, Ling NC, Staehlin T, Crowe P,  
XX  
DR WPI; 2000-224661/19.  
XX  
PT Inducing a Th2 immune response and a persistent systemic immune response  
PT to myelin basic protein, MBP, or a peptide analog of MBP for use in  
PT treating multiple sclerosis, by administering compositions comprising  
PT peptide analogs of MBP.  
XX  
XX Example 10; Fig 8; 112pp; English.  
XX  
XX The present sequence represents a peptide derived from human myelin basic  
XX protein. Myelin basic protein is found in the cytoplasm of human  
XX oligodendroglial cells. Peptide analogue derived from the present  
XX sequence are administered to a patient in need to induce a Th2 immune  
XX response (i.e. production of T cells producing one or more Th2-type  
XX cytokines) and/or a persistent systemic immune response to myelin basic  
XX protein. These peptide analogues are at least seven amino acids long,  
XX derived from residues 83-99 of human myelin basic protein and altered  
XX from the native sequence at least at positions 91, 95 or 97. The peptide

CC analogs are especially useful in the treatment of multiple sclerosis  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
RESULT 2  
AAO20308 standard; peptide; 17 AA.  
AC AAO20308;  
DT 31-MAY-2002 (first entry)  
XX Myelin basic protein (MBP) epitope peptide region 83-99.  
DE  
XX MBP: myelin basic protein; epitope; antiasthmatic; tolerogenic peptide;  
KM dermatological; anti-allergic; neuroprotective; antithyroid; antianemic;  
KM vasotropic; antiinflammatory; immunosuppressive; antidiabetic; class I;  
KM major histocompatibility complex; MHC; class II; autoimmune thyroiditis;  
KM hypersensitivity disorder; antigen; allergy; extrinsic asthma; urticaria;  
KM autoimmune haemolytic anaemia; atopic dermatitis; allergic rhinitis;  
KM autoimmune disease; multiple sclerosis; Grave's disease; sarcoidosis;  
KM systemic sclerosis; polypositis; diabetes; transplant rejection;  
KM antiviral CD8+.  
XX  
XX Unidentified.  
OS  
XX MO200216410-A2.  
PN  
XX 28-FEB-2002.  
PD  
XX 17-AUG-2001; 2001WO-GB003702.  
PF  
XX 21-AUG-2000; 2000GB-00020618.  
PR 14-JUN-2001; 2001GB-00014547.  
XX  
XX (UYBR-) UNITV BRISTOL.  
PA  
PI Wraith DC, Anderson SM, Mazza G, Ponsford M, Streeter HB;  
XX WPI; 2002-292056/33.  
DR  
XX  
XX Selecting tolerogenic peptide useful for treating autoimmune diseases  
PT e.g. multiple sclerosis, involves selecting peptide which binds major  
PT histocompatibility complex class I or II molecule without further  
XX processing.  
XX  
XX Claim 12; Page 28; 55pp; English.  
PS  
XX The invention relates to a method for selecting a tolerogenic peptide,  
CC comprising selecting a peptide which is capable of binding to a major  
CC histocompatibility complex (MHC) class I or II molecule without further  
CC processing. The peptides of the invention are useful for preventing a  
CC disease such as hypersensitivity disorder, and also for treating and/or  
CC preventing a disease in a subject. The method involves identifying an  
CC antigen for the disease, identifying an epitope (antigen processing  
CC independent epitope) for the antigen, and administering the epitope to  
CC the subject. The peptides of the invention are also useful for treating  
CC allergies such as extrinsic asthma, atopic dermatitis, allergic rhinitis,  
CC urticaria, autoimmune diseases such as multiple sclerosis, autoimmune  
CC thyroiditis, Grave's disease, systemic sclerosis, sarcoidosis, autoimmune  
CC haemolytic anaemia, polypositis, diabetes, etc, and transplant  
CC rejection. The peptides are also useful for modifying antiviral CD8+  
CC responses in a tolerogenic fashion. This sequence represents an epitope  
CC of the invention of peptide region 83-99 of Myelin basic protein (MBP)

XX SQ Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
RESULT 3  
AAE26359 standard; peptide; 17 AA.  
XX AAE26359;  
AC AAE26359;  
DT 13-DEC-2002 (first entry)  
XX  
XX Peptide related to myelin basic protein.  
DE  
XX Th2 immune response; myelin basic protein; MBP; vaccine; MS;  
KM multiple sclerosis; antisclerotic.  
XX  
XX Unidentified.  
OS  
XX US6379670-B1.  
PN  
XX 30-APR-2002.  
PD  
XX 19-AUG-1999; 99US-00378244.  
PF  
XX 18-NOV-1994; 94US-00342408.  
PR 20-AUG-1998; 98US-00137759.  
XX  
XX (NEUR-) NEUROCRINE BIOSCIENCES INC.  
PA (NOVS) NOVARTIS AG.  
XX  
XX Gaur A, Conlon P, Ling NC, Staehelin T, Crowe PD;  
XX WPI; 2002-461895/49.  
DR  
XX  
XX Inducing Th2 immune responses to Myelin Basic Protein (MBP) by  
PT administering the MBP peptide analog CGP 77116, useful for treating  
PT Multiple Sclerosis.  
XX  
XX Disclosure; Col 35-36; 49pp; English.  
PS  
XX The present invention relates to a novel method for inducing Th2 immune  
CC responses to Myelin Basic Protein (MBP) or a peptide analogue of MBP in a  
CC patient. The method involves administering a composition comprising the  
CC MBP peptide analogue CGP 77116 (NBI-5788). The method is useful for  
CC treating multiple sclerosis (MS). Sequences of the invention are also  
CC used as vaccines. The present sequence is a peptide related to human MBP  
XX  
XX SQ Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
RESULT 4  
AAE23935 standard; peptide; 17 AA.  
XX AAE23935;  
AC AAE23935;  
XX

DT 10-SEP-2002 (first entry)  
XX Peptide analogue used in the invention.  
DE Autoimmune disease; multiple sclerosis; MS; Jbeta; Cbeta; Vbeta; Dbeta;  
XX immunosuppressive; T-cell receptor; therapy.  
KW Unidentified.  
XX WO200216434-A1.  
XX PD 28-FEB-2002.  
XX PF 22-AUG-2000; 2000WO-US022988.  
XX PR 22-AUG-2000; 2000WO-US022988.  
XX PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX PI Zhang JZ;  
XX DR WPI; 2002-454317/48.  
XX PT A novel peptide used in the treatment of autoimmune disease e.g. multiple  
XX sclerosis.  
PS Example 2; Fig 2; 64pp; English.  
XX The invention relates to a peptide used in the treatment of autoimmune  
XX disease e.g. multiple sclerosis (MS). More particularly, it concerns a T-  
XX cell receptor sequence found in some MS patients and methods for its  
XX detection. T cell receptors comprise alpha and beta chains, with beta  
XX chains comprising the following regions from N-terminus to C-terminus:  
XX Vbeta-Dbeta-Cbeta. T cell receptors naturally vary in the Vbeta-  
XX Dbeta-Jbeta region. The peptides of the invention are used for treating  
XX autoimmune disease e.g multiple sclerosis. The present sequence is a  
XX peptide analogue used in the exemplification of the invention  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVHFFKNIVTPRTP 17  
DB 1 ENPVHFFKNIVTPRTP 17  
RESULT 5  
ABP97941  
ID ABP97941 standard; peptide; 17 AA.  
XX AC ABP97941;  
XX DT 17-JUN-2003 (first entry)  
XX DE Amino acid sequence of a glycopeptide.  
XX KW Glycopeptide; serum; immunosorption column; antibody;  
XX multiple sclerosis.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT Modified-site 1 /note= "H attached"  
XX FT Modified-site 2 /note= "glycosylated residue"  
XX FT Modified-site 17 /note= "OH attached"  
XX PN WO2003009887-A2.

XX 06-FEB-2003.  
XX PD 25-JUL-2002; 2002WO-EP008274.  
XX PF 25-JUL-2001; 2001IT-FI000144.  
XX PR (UYFI-) UNIV FIRENZE.  
XX PA Pinto F, Papini AM, Chelli M, Rovero P, Lotti F;  
XX PI WPI; 2003-312632/30.  
XX DR Immunosorption column, useful for treating multiple sclerosis, contains  
XX PT glycopeptides able to react with disease-specific autoantibodies.  
XX PS Claim 4; Page 6; 13pp; English.  
XX ABP97937-44 represent glycopeptides of a formula given in the  
XX CC specification. The glycopeptides are used to produce columns of the  
XX CC invention. The specification describes immunosorption columns,  
XX CC containing conjugates comprising glycopeptides which are able to  
XX CC recognize antibodies implicated in multiple sclerosis. The column removes  
XX CC harmful antibodies selectively, leaving all other components of the serum  
XX CC unchanged. The column is used to treat multiple sclerosis  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVHFFKNIVTPRTP 17  
DB 1 ENPVHFFKNIVTPRTP 17  
RESULT 6  
ABR56063  
ID ABR56063 standard; peptide; 17 AA.  
XX AC ABR56063;  
XX DT 06-AUG-2003 (first entry)  
XX DE Glycopeptide #5 for diagnosis and treatment of multiple sclerosis.  
XX KW Glycopeptide; neuroprotective; autoantibody; multiple sclerosis.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT Modified-site 2 /note= "Asn(Glc)"  
XX PN WO2003000733-A2.  
XX PD 03-JAN-2003.  
XX PF 19-JUN-2002; 2002WO-EP006767.  
XX PR 22-JUN-2001; 2001IT-FI000114.  
XX PA (UYFI-) UNIV FIRENZE.  
XX PI Papini AM, Chelli M, Rovero P, Lotti F;  
XX DR WPI; 2003-354383/33.  
XX PT Novel glycopeptides comprising a specific tetrapeptide, useful as  
XX PT diagnostic tools for identifying multiple sclerosis.  
XX PS Claim 7; Page 12; 14pp; English.

XX The present invention relates to glycopeptides (ABR56059-ABR56066). The  
CC glycopeptides have high specificity in recognizing autoantibodies  
CC involved in multiple sclerosis pathology, and thus are effectively used  
CC in diagnosis and treatment for multiple sclerosis  
XX  
SQ Sequence 17 AA:  
Query Match 100.0%; Score 94; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
RESULT 7  
AA019672  
ID AA019672 standard; peptide; 17 AA.  
XX  
AC AA019672;  
XX  
DE 28-MAR-2003 (first entry)  
XX  
DE Human myelin basic protein MBP minimal epitope.  
XX  
XX Human; Ig; immunoglobulin; immunotherapy; immune disease; MBP;  
XX Fc epsilon receptor; autoimmune disease; constant region; heavy chain;  
XX antihistaminic; antiallergic; antiinflammatory; dermatological; GE2;  
XX anticholinergic; antineuritic; antidiabetic; neuroprotective;  
XX myelin basic protein; minimal epitope.  
XX  
XX Homo sapiens.  
XX  
XX WO200288317-A2.  
XX  
XX 07-NOV-2002.  
XX  
XX 01-MAY-2002; 2002WO-US013527.  
XX  
XX 01-MAY-2001; 2001US-00847208.  
XX  
XX 24-OCT-2001; 2001US-00000439.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Saxon A, Zhang K, Zhu D;  
XX  
XX MPI; 2003-103456/09.  
XX  
XX New fusion molecules comprising polypeptide sequences that bind to IgG  
XX inhibitory receptor and native IgG receptor, useful for treating IgG-  
XX mediated hypersensitivity reactions, e.g. asthma or allergies, or  
XX autoimmune diseases.  
XX  
XX Claim 23; Page 116; 116pp; English.  
XX  
XX The present invention relates to a fusion molecule comprising a first  
XX polypeptide sequence capable of specific binding to a native IgG  
XX inhibitory receptor consisting of an immune receptor tyrosine-based  
XX inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
XX functionally connected to a second polypeptide sequence capable of  
XX specific binding directly or indirectly to a native IgG receptor  
XX (Fc epsilon receptor). Also provided are nucleotide sequences encoding such a  
XX fusion protein. The fusion molecules and compositions are useful for  
XX treating an IGE-mediated biological response, preferably an IGE-mediated  
XX hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
XX dermatitis, severe food allergies, chronic urticaria, angioedema or  
XX anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
XX type-I diabetes mellitus, or multiple sclerosis, and for preventing of,  
XX or symptoms resulting from, a type I hypersensitivity reaction in a  
XX subject receiving immunotherapy. The present sequence is the human myelin  
XX basic protein minimal epitope which can be used in a fusion protein of

CC the invention  
XX  
SQ Sequence 17 AA:  
Query Match 100.0%; Score 94; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
RESULT 8  
ADE50773  
ID ADE50773 standard; peptide; 17 AA.  
XX  
AC ADE50773;  
XX  
DE 29-JAN-2004 (first entry)  
XX  
DE Wild-type human myelin basic protein peptide analog.  
XX  
XX Human; Th2; immune response; myelin basic protein; peptide analog;  
XX proteolysis; multiple sclerosis; neuroprotective; gene therapy.  
XX  
XX Homo sapiens.  
XX  
XX US2002176866-A1.  
XX  
XX 28-NOV-2002.  
XX  
XX 20-MAR-2002; 2002US-00104973.  
XX  
XX 18-NOV-1994; 94US-00342408.  
XX  
XX 20-AUG-1998; 98US-00137759.  
XX  
XX 19-AUG-1999; 99US-00378244.  
XX  
XX (NEUR-) NEUROCRINE BIOSCIENCES INC.  
XX  
XX Gaur A, Conlon P, Ling NC, Staehelin T, Crowe PD;  
XX  
XX MPI; 2003-615722/58.  
XX  
XX Inducing a Th2 immune response to myelin basic protein or its peptide  
XX analog in a patient, useful for treating multiple sclerosis, comprises  
XX administering an amount of a pharmaceutical composition comprising a  
XX peptide analog.  
XX  
XX Disclosure; SEQ ID NO 3; 52pp; English.  
XX  
XX The invention discloses a method for inducing a Th2 immune response to  
XX myelin basic protein or its peptide analog in a patient, comprising  
XX administering a composition comprising a peptide analog in combination  
XX with a carrier/adjuvant or diluent. The peptide analog comprises at least  
XX 7 amino acids selected from residues 83 to 99 of human myelin basic  
XX protein, where: the L-lysine at position 91, L-arginine at position 97 or  
XX L-threonine at position 95, is altered to another amino acid, and one to  
XX three L-amino acids selected from valine at position 86 or 87, histidine  
XX at position 88, threonine at position 95 or 98, and proline at position  
XX 99 are altered to an amino acid other than the amino acid present in the  
XX native protein at that position or the L-lysine at position 91 is altered  
XX to another amino acid and the N- and/or C-terminal amino acid are altered  
XX to another amino acid, such that upon administration of the peptide  
XX analog in vivo proteolysis is reduced. The peptide analog comprises 7-17  
XX amino acids and one to four additional altered residues. The N-terminal  
XX amino acid is residue 83 of human myelin basic protein. At least one of  
XX the additional L-amino acids selected from residues 83 to 90 and 92 to 99  
XX is substituted with a charged amino acid. The method is useful for  
XX treating multiple sclerosis using peptide analogs of human myelin basic  
XX protein. The sequence presented is the wild-type human myelin basic  
XX protein peptide analog.

SO Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6,1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 ENPVVHFFKNIVTPRTP 17  
1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
RESULT 9  
ADK67704  
ID ADK67704 standard; peptide; 17 AA.  
AC ADK67704;  
XX  
XX  
DT 06-MAY-2004 (first entry)  
DE Human myelin basic protein peptide fragment MBP-1 (aa110-126).  
XX Human; myelin basic protein; vaccine; multiple sclerosis; T cell.  
XX Homo sapiens.  
XX WO2004015070-A2.  
XX 19-FEB-2004.  
XX 06-AUG-2003; 2003WO-US024548.  
XX 08-AUG-2002; 2002US-0402521P.  
XX (BAYU) BAYLOR COLLEGE MEDICINE.  
XX (OPEX-) OPEXA PHARM INC.  
XX Zhang JZ;  
XX WPI; 2004-180654/17.  
XX  
XX  
XX Isolating one or more T cells specific for an antigen of interest  
XX comprises incubating a T cell sample with an antigen, useful for  
XX diagnosing or treating multiple sclerosis, psoriasis, thyroiditis,  
XX diabetes and rheumatoid arthritis.  
XX  
XX Example 1; SEQ ID NO 1; 36pp; English.  
XX  
XX The present invention is direct to methods of isolating antigen specific  
XX T cells, especially T cells specific for self or autoantigens. This  
XX comprises incubating a sample of T cells obtained from a patient with the  
XX antigen and selecting T cells that express one or more of first markers  
XX selected from CD63, CD4, CD25, CD36 and HLA-DR, and one or more second  
XX markers selected from interleukin-2, interferon-gamma, tumour necrosis  
XX factor alpha, interleukin-5, interleukin-10 and interleukin-12. The  
XX methods are useful for isolating autoreactive T cells which play a role  
XX in the pathogenesis of autoimmune diseases. The methods also permit the  
XX diagnosis of autoimmune disease as well as monitoring the progression of  
XX the disease and for monitoring the efficacy of treatment. The methods  
XX allow the preparation of autologous T cell vaccines for the treatment of  
XX T cell related autoimmune diseases. Vaccine preparation involves the  
XX isolation of antigen-specific T cells optionally followed by culturing  
XX steps which allow the expansion of the population of isolated antigen-  
XX specific T cells. An example from the invention describes the isolation  
XX of myelin-reactive T cells for T cell vaccination. Peripheral blood  
XX mononuclear cells were isolated from the blood of multiple sclerosis  
XX patients and incubated with peptides comprising known immunodominant  
XX regions of 3 myelin proteins. These included the present peptide, which  
XX comprises amino acids 110-126 of human myelin basic protein. Cells were  
XX then selected for the expression of gene products indicative of activated  
XX T cells, and myelin-reactive T cells were propagated in culture. The  
XX methods and compositions of the invention are useful for the diagnosis  
XX and/or treatment of autoimmune diseases or T cell associated conditions  
XX such as multiple sclerosis, myasthenia gravis, psoriasis, systemic lupus

CC erythematous, autoimmune thyroiditis, Grave's disease, inflammatory  
CC bowel disease, diabetes and rheumatoid arthritis.  
XX  
XX  
SO Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6,1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 ENPVVHFFKNIVTPRTP 17  
1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
RESULT 10  
ADL18291  
ID ADL18291 standard; peptide; 17 AA.  
AC ADL18291;  
XX  
XX  
DT 20-MAY-2004 (first entry)  
DE Human myelin basic protein (MBP), peptide #2.  
XX  
XX Demyelinating disease; neuron-specific antigen; human;  
XX myelin basic protein; MBP; myelin oligodendrocyte glycoprotein;  
XX myelin associated glycoprotein; MAG; proteolipid protein; PLP;  
XX small heat shock protein; transthyretin; glial fibrillary protein;  
XX S-100 protein; cross-reactive peptide; glutamate receptor;  
XX phosphodiesterase; multiple sclerosis.  
XX  
XX Homo sapiens.  
XX  
XX US2004043431-A1.  
XX 04-MAR-2004.  
XX 29-AUG-2002; 2002US-00233892.  
XX 29-AUG-2002; 2002US-00233892.  
XX (VOUD/) VOUDANI A.  
XX Vojdani A;  
XX  
XX WPI; 2004-313756/29.  
XX  
XX  
XX Diagnosing likelihood and severity of demyelinating disease, by  
XX PT determining antibodies against neuron-specific antigen, comparing level  
XX of detected antibodies with normal level for detecting absence/likelihood  
XX of demyelinating disease.  
XX  
XX  
XX Claim 6; SEQ ID NO 2; 27pp; English.  
XX  
XX The present invention relates to a method of diagnosing the likelihood  
XX and severity of demyelinating diseases. The method involves determining  
XX antibodies against neuron-specific antigen in sample, comparing the level  
XX of antibodies with the normal level of antibodies, where normal level of  
XX antibodies for neuron-specific antigen indicate optimal conditions, lower  
XX than or higher than normal level of antibodies for the antigen indicate  
XX an absence of or a likelihood of demyelinating diseases, respectively.  
XX The neuron-specific antigen is chosen from myelin basic protein (MBP),  
XX myelin oligodendrocyte glycoprotein, myelin associated glycoprotein  
XX (MAG), proteolipid protein (PLP), small heat shock protein,  
XX transthyretin, glial fibrillary protein, S-100 protein, cross-reactive  
XX peptide from dietary protein, cross-reactive peptide from infectious  
XX agent, glutamate receptor, and phosphodiesterase. The immunoassay is an  
XX enzyme linked immunosorbent assay (ELISA) test. The method is useful for  
XX diagnosing the likelihood and severity of demyelinating diseases such as  
XX multiple sclerosis in a patient. The present sequence represents a  
XX peptide from human MBP.  
XX  
XX Sequence 17 AA;

Query Match 100.0%; Score 94; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
| | | | | | | | | | | | | | | | | |  
Db 1 ENPVVHFFKNIVTPRTP 17

## RESULT 11

AAR44116  
ID AAR44116 standard; peptide; 17 AA.

AC AAR44116;  
XX  
DT 25-MAR-2003 (revised)  
DT 09-MAY-1994 (first entry)  
XX

DE Human myelin basic protein residues 86-102.

KW hMBP; suppression; auto immune response; multiple sclerosis;  
KW immunodominant epitope; T-cell proliferation; CD4; T-cells.

XX Homo sapiens.

OS WO9321222-A1.

PD 28-OCT-1993.

PF 09-APR-1993; 93WO-US003369.

PR 09-APR-1992; 92US-00865318.

XX (AUTO-) AUTOIMMUNE INC.

PA Weiner HL, Haefler DA, Miller A, Al-Sabbagh A;

XX WPI; 1993-351657/44.

PT New peptide(s) derived from human myelin basic protein - used for  
PT suppressing auto-immune response, partic. in treating multiple sclerosis.

PS Claim 1; Page 29; 118pp; English.

CC The peptide represents residues 86-102 of human myelin basic protein  
CC (hMBP). The fragment comprises an immunodominant epitope of hMBP which  
CC was identified by overlapping 20-mer oligopeptide sequence analysis using  
CC T-cell line assays. The peptide can be used to stop proliferation of  
CC human T-cells specific for MBP or to elicit active suppression of such T-  
CC cells. They are also used partic. for the treatment of multiple  
CC sclerosis. The peptide is also useful for identifying CD4+ T-cells  
CC reactive with MBP. See also AAR44114-25. (Updated on 25-MAR-2003 to  
CC correct PN field.)

XX Sequence 17 AA.

QY Query Match 94.7%; Score 89; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.4e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NPVVHFFKNIVTPRTP 17  
| | | | | | | | | | | | | | | | | |  
Db 1 NPVVHFFKNIVTPRTP 16

## RESULT 12

AAR95360  
ID AAR95360 standard; peptide; 17 AA.

AC AAR95360;  
XX  
DT 16-DEC-1996 (first entry)  
XX

XX Residues 84-100 of myelin basic protein.

KW Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;  
KW CD4+; T-cell; autoimmune disease; demyelination; central nervous system;  
KW CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;  
KW relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;  
KW diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;  
KW psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;  
KW myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.

XX Synthetic.

OS WO9612737-A2.

PD 02-MAY-1996.

PF 25-OCT-1995; 95WO-US013682.

PR 25-OCT-1994; 94US-00328224.

PR 15-MAR-1995; 95US-00404228.

XX (IMMU-) IMMUNOLOGIC PHARM CORP.

PI Smilek D, Samson M, Gefter M, Hsu D, Shi J, Pallard X, Devaux B;

XX Rothbard J, Franzen H;

XX WPI; 1996-230552/23.

PT Myelin basic derived peptide(s) and analogs - used in the treatment of  
PT Multiple Sclerosis, psoriasis, Graves Disease, etc.

XX Claim 8; Fig 14; 91pp; English.

CC AAR95334-R95374 represent peptides derived from myelin basic protein  
CC (MBP). Immunisation with MBP can be used to induce experimental allergic  
CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+ T-  
CC cell mediated autoimmune disease which results in demyelination of the  
CC central nervous system, resulting in paralysis and other neurological  
CC abnormalities. EAE is a commonly used animal model for human multiple  
CC sclerosis (MS). These sequences can be used in compositions for treating  
CC MS in a mammal. The composition acts to down regulate the autoimmune  
CC response, and may be administered in an amount sufficient to prevent the  
CC onset of symptoms of MS. The compositions may also be used to treat  
CC advanced stage MS, especially relapsing-remitting MS, chronic progressive  
CC MS or benign MS. These peptides may also be used in the treatment of  
CC other diseases involving myelin autoantigens, including diabetes, Graves  
CC disease, myasthenia gravis, Good Pasture's syndrome, psoriasis,  
CC thyroiditis, and rheumatoid arthritis. Peptides derived from other myelin  
CC autoantigens, such as myelin oligodendrocyte protein (MOG), proteolipid  
CC protein (PLP), and myelin associated glycoprotein (MAG) can be used as  
CC alternatives to these MBP peptides in these compositions

XX Sequence 17 AA.

QY Query Match 94.7%; Score 89; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.4e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NPVVHFFKNIVTPRTP 17  
| | | | | | | | | | | | | | | | | |  
Db 1 NPVVHFFKNIVTPRTP 16

## RESULT 13

AAW73601  
ID AAW73601 standard; peptide; 17 AA.

AC AAW73601;  
XX  
DT 18-MAR-1999 (first entry)  
XX

DE Human myelin basic protein fragment.

encephalic protein and peptides.",  
 Science 179:478-480(1973).  
 -1- FUNCTION: Is, with PIP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bilayers. Each splice variant and charge isomer may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).  
 -1- SUBUNIT: Homodimer (By similarity).  
 -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.  
 -1- ALTERNATIVE PRODUCTS:  
 Event-Alternative splicing; Named isoforms=4;  
 Comment=Additional isoforms seem to exist;  
 Name=1; Synonyms=21.5 kDa;  
 IsoId=P02688-1; Sequence=Displayed;  
 Name=2; Synonyms=18.5 kDa;  
 IsoId=P02688-2; Sequence=VSP\_003321;  
 Name=3; Synonyms=17 kDa;  
 IsoId=P02688-3; Sequence=VSP\_003322;  
 Name=4; Synonyms=14 kDa;  
 IsoId=P02688-4; Sequence=VSP\_003321; VSP\_003322;  
 TISSUE SPECIFICITY: Found in both the central and the peripheral nervous system.  
 -1- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.  
 -1- PTM: Arg-130 was found to be 44% monomethylated and 11% symmetrically dimethylated.  
 -1- SIMILARITY: Belongs to the myelin basic protein family.  
 -----  
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 -----  
 EMBL; AJ132895; CA10804.1; -;  
 EMBL; AJ132896; CA10805.1; -;  
 EMBL; AJ132897; CA10806.1; -;  
 EMBL; AJ132898; CA10807.1; -;  
 EMBL; M25889; AAA1575.1; -;  
 EMBL; K00512; -; NOT\_ANNOTATED\_CDS.  
 EMBL; X72392; -; NOT\_ANNOTATED\_CDS.  
 PIR; B24351; MBRTS.  
 HSSP; P02686; IQCL.  
 DR RGD; 3054; MBP.  
 DR InterPro: IPR000548; Myelin\_BP.  
 DR Pfam; PR01669; Myelin\_MBP; I.  
 DR PRINTS; PR00212; MYELINBP.  
 DR ProDom; PD004542; Myelin\_BP; 1.  
 DR PROSITE; PS00569; MYELIN\_MBP; 1.  
 ACetylation; Alternative splicing; Autoimmune encephalomyelitis; Citrullination; Direct protein sequencing; Methylation; Myelin; KM Phosphorylation; Structural protein.  
 KM INIT\_MET 0 0  
 FT MOD\_RES 1 7 N-acetylalanine.  
 FT MOD\_RES 7 7 Phosphoserine (By similarity).  
 FT MOD\_RES 25 25 Citrulline (By similarity).  
 FT MOD\_RES 31 31 Citrulline (By similarity).  
 FT MOD\_RES 56 56 Phosphoserine (By similarity).  
 FT MOD\_RES 121 121 Phosphothreonine (By similarity).  
 FT MOD\_RES 126 126 Deamidated glutamine (partial) (By similarity).  
 FT MOD\_RES 130 130 Omega-N-methylarginine (partial).  
 FT MOD\_RES 130 130 Symmetric dimethylarginine (partial).  
 FT MOD\_RES 138 138 Phosphoserine (By similarity).  
 FT MOD\_RES 153 153 Citrulline (By similarity).  
 FT MOD\_RES 171 171 Deamidated glutamine (partial) (By similarity).  
 FT

FT MOD\_RES 183 183 Citrulline (By similarity).  
 FT MOD\_RES 185 185 Phosphoserine (By similarity).  
 FT MOD\_RES 189 189 Phosphoserine (By similarity).  
 FT MOD\_RES 194 194 Citrulline (By similarity).  
 FT VARSPPLIC 59 84 Missing (in isoform 2 and isoform 4).  
 FT VARSPPLIC 140 180 /FTId=VSP\_003322.  
 FT CONFLICT 46 47 Missing (in isoform 3 and isoform 4).  
 FT CONFLICT 191 191 /FTId=VSP\_003322.  
 FT CONFLICT 191 191 SC -> GS (in Ref. 6).  
 FT SEQUENCE 194 AA; 21371 MW; 68FB399C250B4C50 CRC64;  
 SQ  
 Query Match 100.0%; Score 94; DB 1; Length 194;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ENPVVHFFKNIVTPRTP 17  
 DB 106 ENPVVHFFKNIVTPRTP 122  
 PRT; 203 AA.  
 Q65ZS4 PRELIMINARY;  
 ID Q65ZS4  
 AC Q65ZS4;  
 DT 25-OCT-2004 (TREMBLrel. 28, Created)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE Myelin basic protein.  
 DE Name=MBP;  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP MEDLINE=86259714; PubMed=2425357;  
 RA Kamholz J., de Ferreira F., Puckett C., Lazzarini R.;  
 RT "Identification of three forms of human myelin basic protein by cDNA cloning";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:4962-4966(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96128281; PubMed=8544862; DOI=10.1016/0161-5890(95)00066-6;  
 RA Nye S.H., Pelfrey C.M., Burkitt J.J., Voskuhl R.R., Lenardo M.J.,  
 RA Mueller J.P.;  
 RT "Purification of immunologically active recombinant 21.5 kDa isoform of human myelin basic protein";  
 RL Mol. Immunol. 32:1131-1141(1995).  
 DR EMBL; LA1657; AAC1944.1; -;  
 DR InterPro: IPR000548; Myelin\_BP.  
 DR Pfam; PR01669; Myelin\_MBP; I.  
 DR PRINTS; PR00212; MYELINBP.  
 DR ProDom; PD004542; Myelin\_BP; 1.  
 DR PROSITE; PS00569; MYELIN\_MBP; 1.  
 SQ SEQUENCE 203 AA; 22316 MW; C21A7D718FC2D30F CRC64;  
 Query Match 100.0%; Score 94; DB 2; Length 203;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ENPVVHFFKNIVTPRTP 17  
 DB 110 ENPVVHFFKNIVTPRTP 126  
 PRT; 250 AA.  
 AC P04370; Q01585; Q03139; Q03176; Q61835; Q61837; Q99KE4; Q9QWP1;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 25-JAN-2005 (Rel. 46, Last annotation update)  
 RESULT 13  
 MBP\_MOUSE  
 ID MBP\_MOUSE STANDARD; PRT; 250 AA.  
 AC P04370; Q01585; Q03139; Q03176; Q61835; Q61837; Q99KE4; Q9QWP1;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 25-JAN-2005 (Rel. 46, Last annotation update)

- DE Myelin basic protein (MBP) (Myelin A1 protein).  
OS Name=Mbp; Synonyms=Shi;  
CN Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RC MEDLINE=93186801; PubMed=7680345;  
RA Campagnoni A.T., Pridyl T.M., Campagnoni C.W., Kampf K.,  
RA Amur-Umarjee S., Landry C.F., Handley V.W., Newman S., Garbay B.,  
RA Kitamura K.;  
RT "Structure and developmental regulation of Ggll1-amp, a 105-kilobase  
RT gene that encompasses the myelin basic protein gene and is expressed  
RT in cells in the oligodendrocyte lineage in the brain.";  
RL J. Biol. Chem. 268:4930-4938(1993).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC STRAIN=C57BL/6; TISSUE=Bone marrow;  
RC MEDLINE=93057537; PubMed=1279125;  
RA Grima B., Zelenika D., Pessac B.;  
RT "A novel transcript overlapping the myelin basic protein gene";  
RL J. Neurochem. 59:2318-2323(1992).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 8).  
RC MEDLINE=86079555; PubMed=2416470; DOI=10.1016/0092-8674(85)90245-4;  
RA de Ferra F., Singh H., Hudson L., Kamholz J., Puckett C., Moliniaux S.,  
RA Lazzerini R.A.;  
RT "Alternative splicing accounts for the four forms of myelin basic  
RT protein.";  
RL Cell 43:721-727(1985).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 5).  
RC MEDLINE=85524913; PubMed=2410136;  
RA Takehashi N., Roach A., Teplov D.B., Prusiner S.B., Hood L.E.;  
RT "Cloning and characterization of the myelin basic protein gene from  
RT mouse: one gene can encode both 14 kd and 18.5 kd MBPs by alternate  
RT use of exons.";  
RL Cell 42:139-148(1985).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORMS 6 AND 7), AND SEQUENCE OF 9-194 FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Brain;  
RC MEDLINE=87118269; PubMed=2433693;  
RA Newman S., Kitamura K., Campagnoni A.T.;  
RT "Identification of a cDNA coding for a fifth form of myelin basic  
RT protein in mouse.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:886-890(1987).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM 8).  
RC PubMed=1692584;  
RA Kitamura K., Newman S.L., Campagnoni C.W., Verdi J.M., Mohandas T.,  
RA Handley V.W., Campagnoni A.T.;  
RT "Expression of a novel transcript of the myelin basic protein gene.";  
RL J. Neurochem. 54:2032-2041(1990).  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 8).  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Oato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gyojibori T.,  
RA Balarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schimi L.M., Kanaphi A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusci V., Chotia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Guetlich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedierski R.M., Kling B.L.,  
RA Kongsaya K., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Malais K., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Sempé C.A., Setou M., Shinada K.,  
RA Sultana K., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wegner T., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,  
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carinci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Maki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney B., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs";  
RL Nature 420:563-573(2002).  
RN [8]  
RP SEQUENCE FROM N.A. (ISOFORM 9).  
RC TISSUE=Breast tumor;  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [9]  
RP SEQUENCE OF 135-157 FROM N.A.  
RC MEDLINE=89252919; PubMed=2470651; DOI=10.1016/0378-1119(89)90380-6;  
RA Miura M., Tamura T.A., Aoyama A., Mikoshiba K.;  
RT "The promoter elements of the mouse myelin basic protein gene function  
RT efficiently in NG108-15 neuronal/glia cells.";  
RL Gene 75:31-38(1989).  
RN [10]  
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 4; 6 AND 9).  
RC MEDLINE=86259714; PubMed=2425357;  
RA Kamholz J., de Ferra F., Puckett C., Lazzerini R.A.;  
RT "Identification of three forms of human myelin basic protein by cDNA  
RT cloning.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:4962-4966(1986).  
RN [11]  
RP SEQUENCE OF 193-222 FROM N.A.  
RC MEDLINE=84119431; PubMed=6198644;  
RA Zeller N.K., Hunkeler M.J., Campagnoni A.T., Sprague J.,  
RA Lazzerini R.A.;  
RT "Characterization of mouse myelin basic protein messenger RNAs with a  
RT myelin basic protein cDNA clone.";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:18-22(1984).  
RN [12]  
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 10 AND 11).  
RC TISSUE=spinal cord;  
RC MEDLINE=91162193; PubMed=1705957;  
RA Aruga J., Okano H., Mikoshiba K.;  
RT "Identification of the new isoforms of mouse myelin basic protein: the  
RT existence of exon 5a.";  
RL J. Neurochem. 56:1222-1226(1991).  
RN [13]  
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 12 AND 13).  
RC TISSUE=Embryonic brain;  
RC MEDLINE=93203893; PubMed=7681106;





[8] RP SEQUENCE OF 135-192 FROM N.A.  
 RX MEDLINE=90152679; PubMed=1689270;  
 RA Boylan K.B., Ayres T.M., Popko B., Takahashi N., Hood L.E.,  
 RA Prusiner S.B.;  
 RT "Repetitive DNA (TTGG)n 5' to the human myelin basic protein gene: a  
 RT new form of oligonucleotide repetitive sequence showing length  
 RT polymorphism.";  
 RL Genomics 6:16-22(1990).  
 RN [9]  
 RP SEQUENCE OF 179-222 (ISOFORM 5), AND REVISIONS.  
 RA Shapira R., McKenally S.S., Chou F., Kibler R.F.;  
 RT "encephalitogenic fragment of myelin basic protein. Amino acid  
 RT sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";  
 RL J. Biol. Chem. 246:4630-4640(1971).  
 RN [10]  
 RP SEQUENCE OF 135-178 AND 224-304 (ISOFORM 3), AND MASS SPECTROMETRY.  
 RX MEDLINE=86280476; PubMed=2426402;  
 RA Scoble H.A., Whitaker J.N., Blemann K.;  
 RT "Analysis of the primary sequence of human myelin basic protein  
 RT peptides 1-44 and 90-170 by fast atom bombardment mass spectrometry.";  
 RL J. Neurochem. 47:614-616(1986).  
 RN [11]  
 RP SEQUENCE OF 148-304 (ISOFORM 5), AND CITRULLINATION OF C8.  
 RC TISSUE=Brain;  
 RX MEDLINE=89174797; PubMed=2466844;  
 RA Wood D.D., Moscarello M.A.;  
 RT "The isolation, characterization, and lipid-aggregating properties of  
 RT a citrulline containing myelin basic protein.";  
 RL J. Biol. Chem. 264:5121-5127(1989).  
 RN [12]  
 RP SEQUENCE OF 179-223 (ISOFORM 5), AND MASS SPECTROMETRY.  
 RX MEDLINE=84185608; PubMed=6201481;  
 RA Gibson B.W., Gilliom R.D., Whitaker J.N., Blemann K.;  
 RT "Amino acid sequence of human myelin basic protein peptide 45-89 as  
 RT determined by mass spectrometry.";  
 RL J. Biol. Chem. 259:5028-5031(1984).  
 RN [13]  
 RP SEQUENCE OF 246-269 (ISOFORM 3), AND ENCEPHALITIGENIC PEPTIDE.  
 RX MEDLINE=71088405; PubMed=4099924;  
 RA Lennon V.A., Wilks A.V., Carnegie P.R.;  
 RT "Immunologic properties of the main encephalitogenic peptide from the  
 RT basic protein of human myelin.";  
 RL J. Immunol. 105:1223-1230(1970).  
 RN [14]  
 RP SEQUENCE OF 156-172 AND 302-304, AND CHARACTERIZATION OF C8.  
 RC TISSUE=Brain;  
 RX MEDLINE=96604793; PubMed=7574672; DOI=10.1006/abbi.1995.1449;  
 RA Boulas C., Pang H., Mastroratti F., Moscarello M.A.;  
 RT "The isolation and characterization of four myelin basic proteins from  
 RT the unbound fraction during CMS2 chromatography.";  
 RL Arch. Biochem. Biophys. 322:174-182(1995).  
 RN [15]  
 RP PARTIAL SEQUENCE.  
 RC TISSUE=Brain;  
 RX PubMed=7685161;  
 RA Proost P., Van Damme J., Opdenakker G.;  
 RT "Leukocyte gelatinase B cleavage releases encephalitogens from human  
 RT myelin basic protein.";  
 RL Biochem. Biophys. Res. Commun. 192:1175-1181(1993).  
 RN [16]  
 RP METHYLATION.  
 RX MEDLINE=72066401; PubMed=5128665;  
 RA Baldwin G.S., Carnegie P.R.;  
 RT "Isolation and partial characterization of methylated arginines from  
 RT the encephalitogenic basic protein of myelin.";  
 RL Biochem. J. 123:69-74(1971).  
 RN [17]  
 RP STRUCTURE OF 135-148 BY NMR.  
 RX MEDLINE=95377296; PubMed=7544282;  
 RA Mendz G.L., Barden J.A., Martenson R.E.;  
 RT "Conformation of a tetradecapeptide epitope of myelin basic protein.";  
 RL Eur. J. Biochem. 231:659-666(1995).

RN [18]  
 RP 3D-STRUCTURE MODELING OF 135-279 (ISOFORM 5).  
 RX MEDLINE=97172499; PubMed=9020143; DOI=10.1074/jbc.272.7.4269;  
 RA Riddale R.A., Beniac D.R., Tompkins T.A., Moscarello M.A., Harauz G.;  
 RT "Three-dimensional structure of myelin basic protein. II. Molecular  
 RT modeling and considerations of predicted structures in multiple  
 RT sclerois.";  
 RL J. Biol. Chem. 272:4269-4275(1997).  
 RN [19]  
 RP FUNCTION: The classic group of MBP isoforms (isoforms 4-14) are  
 CC with PLP the most abundant protein components of the myelin  
 CC membrane in the CNS. They have a role in both its formation and  
 CC stabilization. The smaller isoforms might have an important role  
 CC in remyelination of demyelinated axons in multiple sclerosis. The non-  
 CC classic group of MBP isoforms (isoforms 1-3/Golli-MBP) may  
 CC preferentially have a role in the early developing brain long  
 CC before myelination, maybe as components of transcriptional  
 CC complexes, and may also be involved in signaling pathways in T-  
 CC cells and neural cells. Differential splicing events combined to  
 CC optional posttranslational modifications give a wide spectrum of  
 CC isoforms, each of them having maybe a specialized function.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=6;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=1; Synonyms=Golli-MBP1, HOG7;  
 CC IsoId=P02686-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Golli-MBP2, HOG5;  
 CC IsoId=P02686-2; Sequence=VSP\_003311;  
 CC Name=3; Synonyms=MBP1, 21.5 kDa;  
 CC IsoId=P02686-3; Sequence=VSP\_003308, VSP\_003309;  
 CC Name=4; Synonyms=MBP2, 20.2 kDa;  
 CC IsoId=P02686-4; Sequence=VSP\_003308, VSP\_003309, VSP\_003310;  
 CC Name=5; Synonyms=MBP3, 18.5 kDa;  
 CC IsoId=P02686-5; Sequence=VSP\_003308;  
 CC Name=6; Synonyms=MBP4, 17.2 kDa;  
 CC IsoId=P02686-6; Sequence=VSP\_003308, VSP\_003310;  
 CC -1- TISSUE SPECIFICITY: MBP isoforms are found in both the central and  
 CC the peripheral nervous system, whereas Golli-MBP isoforms are  
 CC expressed in fetal thymus, spleen and spinal cord, as well as in  
 CC cell lines derived from the immune system.  
 CC -1- DEVELOPMENTAL STAGE: Expression turns on abruptly in fetus of 14  
 CC

Query Match 100.0%; Score 94; DB 1; Length 304;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVPTPTP 17  
 |||||||||||||  
 DB 217 ENPVVHFFKNITVPTPTP 233

RESULT 15  
 MBP\_CHICK  
 ID\_MBP\_CHICK STRAND; PRT; 173 AA.  
 AC P15720;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Myelin basic protein (MBP).  
 GN Name=MBP;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OK NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC STRAIN=White Leghorn; TISSUE=Optic lobe;  
 RX MEDLINE=89358239; PubMed=2475444;  
 RA Zopf D., Sonntag H., Betz H., Gundelfinger E.D.;  
 RT "Developmental accumulation and heterogeneity of myelin basic protein  
 RT transcripts in the chick visual system.";

Search completed: June 7, 2005, 09:01:30  
Job time : 10.3679 secs

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RL  GIa 2:241-249(1989).
CC  -1- FUNCTION: Is, with PLP, the most abundant protein component of the
CC  myelin membrane in the CNS. Has a role in both the formation and
CC  stabilization of this compact multilayer arrangement of bilayers.
CC  Each splice variant and charge isomer may have a specialized
CC  function in the assembly of an optimized, biochemically functional
CC  myelin membrane (By similarity).
CC  -1- SUBUNIT: Homodimer (By similarity).
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
CC  -1- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=2;
CC  Comment=Additional isoforms seem to exist;
CC  Name=1;
CC  IsoId=P15720-1; Sequence=Displayed;
CC  Note=Major isoform;
CC  Name=2;
CC  IsoId=P15720-2; Sequence=VSP_003323;
CC  -1- DEVELOPMENTAL STAGE: In the optic lobe, first detected at
CC  embryonic day 14. Expression strongly increases between embryonic
CC  days 16 and 18, reaches a maximum at postnatal day 1, and then
CC  declines again to the adult level.
CC  -1- PTM: As in other animals, several charge isomers may be produced
CC  as a result of optional posttranslational modifications, such as
CC  phosphorylation of serine or threonine residues, deamidation of
CC  glutamine or asparagine residues, citrullination and methylation
CC  of arginine residues.
CC  -1- SIMILARITY: Belongs to the myelin basic protein family.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X17103; CAA34959.1; -.
DR  PIR; S08535; S08535.
DR  HSSP; P02686; 1OCL.
DR  InterPro; IPR000548; Myelin_BP.
DR  Pfam; PF01669; Myelin_MBP; 1.
DR  PRINTS; PR00212; MYELINMBP.
DR  ProDom; PD004542; Myelin_BP; 1.
DR  PROSITE; PS00569; MYELIN_MBP; 1.
KW  Acetylation; Alternative splicing; Citrullination; Methylation;
KW  Myelin; Phosphorylation; Structural protein.
FT  INIT MET      0      0
FT  MOD_RES      1      1
FT  MOD_RES      7      7
FT  MOD_RES     24     24
FT  MOD_RES     29     29
FT  MOD_RES     96     96
FT  MOD_RES    101    101
FT  MOD_RES     105    105
FT  MOD_RES     113    113
FT  MOD_RES     146    146
FT  MOD_RES     164    164
FT  MOD_RES     168    168
FT  MOD_RES     173    173
FT  MOD_RES     174    174
FT  VARSPLIC     104    114
FT  VARSPLIC     104    114
SQ  SEQUENCE      173 AA; 18677 MW;  ABFE70D4C9CF019D CRC64;
Query Match      92.6%; Score 87; DB 1; Length 173;
Best Local Similarity 88.2%; Pred. No. 2.1e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 ENPVVHFFKNIIVTPRTP 17
DB 81 DNPVHFFKNIIVSPRTP 97
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 09:37:21 ; Search time 143 Seconds  
(without alignments)  
42.821 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94

Sequence: 1 ENPVVHFFKNIVTPRTP 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues 263935

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 17  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: Published Applications\_AA:\*

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3: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*

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19: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	17	US-10-104-973-13	Sequence 3, Appl1
2	94	100.0	17	US-10-000-439-13	Sequence 13, Appl1
3	94	100.0	17	US-10-362-264-1	Sequence 1, Appl1
4	94	100.0	17	US-10-233-892A-2	Sequence 2, Appl1
5	94	100.0	17	US-10-482-044-5	Sequence 5, Appl1
6	87	92.6	17	US-09-813-463A-13	Sequence 13, Appl1
7	87	92.6	17	US-09-813-463A-13	Sequence 13, Appl1
8	82	87.2	15	US-09-909-460-37	Sequence 37, Appl1
9	82	87.2	15	US-09-847-172-41	Sequence 41, Appl1
10	82	87.2	15	US-09-872-836-37	Sequence 37, Appl1
11	82	87.2	15	US-09-739-466C-5	Sequence 5, Appl1
12	82	87.2	15	US-10-152-654-11	Sequence 11, Appl1

13	82	87.2	15	14	US-10-056-583-1	Sequence 1, Appl1
14	82	87.2	15	14	US-10-239-313A-142	Sequence 142, App
15	82	87.2	15	14	US-10-362-264-5	Sequence 5, Appl1
16	82	87.2	15	15	US-10-404-679-11	Sequence 11, Appl1
17	82	87.2	15	15	US-10-406-783-1	Sequence 1, Appl1
18	82	87.2	15	15	US-10-406-783-2	Sequence 2, Appl1
19	82	87.2	15	16	US-10-617-568-26	Sequence 26, Appl1
20	79	84.0	15	14	US-10-056-583-69	Sequence 69, Appl1
21	79	84.0	15	14	US-10-239-313A-144	Sequence 144, App
22	79	84.0	15	14	US-10-239-313A-145	Sequence 145, App
23	78	83.0	15	14	US-10-239-313A-125	Sequence 125, App
24	78	83.0	15	14	US-10-239-313A-126	Sequence 126, App
25	78	83.0	15	14	US-10-239-313A-136	Sequence 136, App
26	78	83.0	15	14	US-10-239-313A-137	Sequence 137, App
27	77	81.9	15	14	US-10-239-313A-134	Sequence 134, App
28	77	81.9	15	14	US-10-239-313A-138	Sequence 138, App
29	77	81.9	15	14	US-10-239-313A-141	Sequence 141, App
30	77	81.9	15	14	US-10-362-264-4	Sequence 4, Appl1
31	76	80.9	14	13	US-10-015-540-3	Sequence 3, Appl1
32	76	80.9	15	14	US-10-239-313A-127	Sequence 127, App
33	76	80.9	15	14	US-10-239-313A-132	Sequence 6, Appl1
34	76	80.9	15	14	US-10-362-264-6	Sequence 6, Appl1
35	76	80.9	15	16	US-10-617-568-18	Sequence 18, Appl1
36	76	80.9	15	16	US-10-617-568-27	Sequence 27, Appl1
37	76	80.9	16	13	US-10-103-395-3	Sequence 3, Appl1
38	76	80.9	16	15	US-10-149-138-4381	Sequence 4381, Ap
39	76	80.9	16	15	US-10-149-135-2321	Sequence 2321, Ap
40	76	80.9	16	16	US-10-149-138-4381	Sequence 4381, Ap
41	76	80.9	17	16	US-10-475-706-4	Sequence 4, Appl1
42	75	79.8	17	13	US-10-104-973-6	Sequence 6, Appl1
43	74	78.7	15	14	US-10-239-313A-118	Sequence 118, App
44	74	78.7	15	14	US-10-239-313A-130	Sequence 130, App
45	74	78.7	15	14	US-10-239-313A-131	Sequence 131, App

#### ALIGNMENTS

RESULT 1

US-10-104-973-3

Sequence 3, Application US/10104973

Publication No. US20020176866A1

GENERAL INFORMATION:

APPLICANT: Gaur, Amitabh

APPLICANT: Conlon, Paul J.

APPLICANT: Ling, Nicholas C.

APPLICANT: Staehlin, Theophil

TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING

TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN

FILE REFERENCE: 690068.405C4

CURRENT APPLICATION NUMBER: US/10104,973

CURRENT FILING DATE: 2002-03-20

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 17

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Solid Phase

US-10-104-973-3

Query Match 100.0%; Score 94; DB 13; Length 17;  
Best local Similarity 100.0%; Pred. No. 4.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17

RESULT 2  
US-10-000-439-13  
; Sequence 13, Application US/10000439  
; Publication No. US20030064063A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
; TREATMENT OF IMMUNE DISEASES  
; FILE REFERENCE: UC067.004A  
; CURRENT APPLICATION NUMBER: US/10/000,439  
; CURRENT FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 09/847,208  
; PRIOR FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-000-439-13

Query Match 100.0%; Score 94; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
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DB 1 ENPVVHFFKNIVTPRTP 17

RESULT 3  
US-10-362-264-1  
; Sequence 1, Application US/10362264  
; Publication No. US20030191063A1  
; GENERAL INFORMATION:  
; APPLICANT: Wraith, David  
; APPLICANT: Anderson, Stephen  
; APPLICANT: Mazza, Graziella  
; APPLICANT: Ponsford, Mary  
; APPLICANT: Streeter, Heather  
; APPLICANT: The University of Bristol  
; TITLE OF INVENTION: PEPTIDE SELECTION METHOD  
; FILE REFERENCE: 1433 004US1  
; CURRENT APPLICATION NUMBER: US/10/362,264  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/GB01/03702  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 0020618.5  
; PRIOR FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: 0114547.3  
; PRIOR FILING DATE: 2001-06-14  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-362-264-1

Query Match 100.0%; Score 94; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
| | | | | | | | | | | | | | | | | | |  
DB 1 ENPVVHFFKNIVTPRTP 17

RESULT 4  
US-10-233-892A-2  
; Sequence 2, Application US/10233892A  
; Publication No. US20040043431A1  
; GENERAL INFORMATION:

; APPLICANT: Vojdani, Aristo  
; TITLE OF INVENTION: DIAGNOSIS OF MULTIPLE SCLEROSIS AND  
; TITLE OF INVENTION: OTHER DEMYELINATING DISEASES  
; FILE REFERENCE: IMSMS.001A  
; CURRENT APPLICATION NUMBER: US/10/233,892A  
; CURRENT FILING DATE: 2002-08-29  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Human Myelin Binding Protein Sequence 83-89  
US-10-233-892A-2

Query Match 100.0%; Score 94; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
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DB 1 ENPVVHFFKNIVTPRTP 17

RESULT 5  
US-10-482-044-5  
; Sequence 5, Application US/10482044  
; Publication No. US20040235713A1  
; GENERAL INFORMATION:  
; APPLICANT: Anna Maria PAPINI et al  
; TITLE OF INVENTION: Glycopeptides, their preparation and use in the diagnosis or  
; TITLE OF INVENTION: therapeutic treatment of multiple sclerosis  
; FILE REFERENCE: 2784 PTWO  
; CURRENT APPLICATION NUMBER: US/10/482,044  
; CURRENT FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: PCT/EP 02/06767  
; PRIOR FILING DATE: 2002-06-19  
; PRIOR APPLICATION NUMBER: FI2001A000114  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: glycopeptide  
; NAME/KEY: CARBOHYD  
; LOCATION: (2)..(2)  
; OTHER INFORMATION: the carbohydrate is beta-D-glucopyranosyl  
US-10-482-044-5

Query Match 100.0%; Score 94; DB 16; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
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DB 1 ENPVVHFFKNIVTPRTP 17

RESULT 6  
US-09-813-463A-13  
; Sequence 13, Application US/09813463A  
; Patent No. US20020147303A1  
; GENERAL INFORMATION:  
; APPLICANT: WARREN, KENNETH G.  
; APPLICANT: CATZ, INGRID  
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND  
; TITLE OF INVENTION: THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO  
; TITLE OF INVENTION: MULTIPLE SCLEROSIS PATIENTS

FILE REFERENCE: 098810/027 8740  
CURRENT APPLICATION NUMBER: US/09/813,463A  
CURRENT FILING DATE: 2002-01-11  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 13  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-813-463A-13

Query Match 92.6%; Score 87; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRT 16  
DB 2 ENPVVHFFKNIVTPRT 17

RESULT 7  
US-09-813-463A-13  
Sequence 13, Application US/09813463A  
Publication No. US20040072991A9  
GENERAL INFORMATION:  
APPLICANT: WARREN, KENNETH G.  
APPLICANT: CATZ, INGRID  
TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND  
TITLE OF INVENTION: THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO  
FILE REFERENCE: 098810/027 8740  
CURRENT APPLICATION NUMBER: US/09/813,463A  
CURRENT FILING DATE: 2002-01-11  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 13  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-813-463A-13

Query Match 92.6%; Score 87; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRT 16  
DB 2 ENPVVHFFKNIVTPRT 17

RESULT 8  
US-09-909-460-37  
Sequence 37, Application US/09909460  
Publication No. US20020182258A1  
GENERAL INFORMATION:  
APPLICANT: Lunsford, Lynn B.  
APPLICANT: Putnam, David  
APPLICANT: Hedley, Mary Lynn  
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC  
FILE REFERENCE: 08191/014001  
CURRENT APPLICATION NUMBER: US/09/909,460  
CURRENT FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27  
NUMBER OF SEQ ID NOS: 114  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 37  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-909-460-37

Query Match 87.2%; Score 82; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPR 15  
DB 1 ENPVVHFFKNIVTPR 15

RESULT 9  
US-09-847-172-41  
Sequence 41, Application US/09847172  
Publication No. US20030007978A1  
GENERAL INFORMATION:  
APPLICANT: OREGON HEALTH AND SCIENCES UNIVERSITY  
APPLICANT: BURREWS, GREGORY G.  
APPLICANT: VANDENBARK, ARTHUR A.  
TITLE OF INVENTION: RECOMBINANT MHC MOLECULES USEFUL FOR MANIPULATION OF ANTIGEN-SPECI  
FILE REFERENCE: 899-58137  
CURRENT APPLICATION NUMBER: US/09/847,172  
CURRENT FILING DATE: 2001-05-01  
PRIOR APPLICATION NUMBER: US 60/200,942  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: US 09/153,586  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: US 60/064,555  
PRIOR FILING DATE: 1997-10-10  
PRIOR APPLICATION NUMBER: US 60/064,552  
PRIOR FILING DATE: 1997-09-16  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 41  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificial peptide  
US-09-847-172-41

Query Match 87.2%; Score 82; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPR 15  
DB 1 ENPVVHFFKNIVTPR 15

RESULT 10  
US-09-872-836-37  
Sequence 37, Application US/09872836  
Publication No. US20040142475A1  
GENERAL INFORMATION:  
APPLICANT: Bartman, Shikha P.  
APPLICANT: McKeever, Una  
APPLICANT: Hedley, Mary Lynne  
TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS  
FILE REFERENCE: 08191-018001  
CURRENT APPLICATION NUMBER: US/09/872,836  
CURRENT FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: US 60/208,830  
PRIOR FILING DATE: 2000-06-02  
NUMBER OF SEQ ID NOS: 120  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 37  
LENGTH: 15

TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-872-836-37

Query Match 87.2%; Score 82; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVPR 15  
Db 1 ENPVVHFFKNITVPR 15

RESULT 11

US-09-739-466C-5  
Sequence 5, Application US/09739466C  
Publication No. US20050107585A1  
GENERAL INFORMATION:  
APPLICANT: MURRAY, JOSEPH S  
APPLICANT: SIHMAN, TERUNA J  
APPLICANT: HU, YONGBO  
TITLE OF INVENTION: SIGNAL-1/SIGNAL-2 BIFUNCTIONAL PEPTIDE INHIBITORS  
FILE REFERENCE: 23902-08805  
CURRENT APPLICATION NUMBER: US/09/739,466C  
CURRENT FILING DATE: 2000-12-18  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: Patenlin Ver. 3.2  
SEQ ID NO 5  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-739-466C-5

Query Match 87.2%; Score 82; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVPR 15  
Db 1 ENPVVHFFKNITVPR 15

RESULT 12

US-10-152-654-11  
Sequence 11, Application US/10152654  
Publication No. US20020137681A1  
GENERAL INFORMATION:  
APPLICANT: Steinman, Lawrence  
APPLICANT: Ruiz, Pedro  
TITLE OF INVENTION: Treatment of Demyelinating Autoimmune  
TITLE OF INVENTION: Disease with Ordered Peptides  
FILE REFERENCE: STAN-129  
CURRENT APPLICATION NUMBER: US/10/152,654  
CURRENT FILING DATE: 2002-05-20  
PRIOR APPLICATION NUMBER: US/09/606,254  
PRIOR FILING DATE: 2000-06-28  
PRIOR APPLICATION NUMBER: 60/142,479  
PRIOR FILING DATE: 1999-07-06  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Peptide  
US-10-152-654-11

Query Match 87.2%; Score 82; DB 13; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVPR 15

Db 1 ENPVVHFFKNITVPR 15

RESULT 13  
US-10-056-583-1  
Sequence 1, Application US/10056583  
Publication No. US20030064915A1

GENERAL INFORMATION:  
APPLICANT: Presidents and Fellows of Harvard College  
APPLICANT: Strominger, Jack L.  
APPLICANT: Fridkis-Hareli, Masha  
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
FILE REFERENCE: 24655-017  
CURRENT APPLICATION NUMBER: US/10/056,583  
CURRENT FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: 60/263,569  
PRIOR FILING DATE: 2001-01-24  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Immunodominant peptide of MBP, recognized by  
NAME/KEY: DOMAIN  
LOCATION: 85 - 99  
US-10-056-583-1

Query Match 87.2%; Score 82; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVPR 15  
Db 1 ENPVVHFFKNITVPR 15

RESULT 14

US-10-239-313A-142  
Sequence 142, Application US/10239313A  
Publication No. US20030175285A1  
GENERAL INFORMATION:  
APPLICANT: KLINGNER - HAMOUR, Christine  
APPLICANT: CORVAIA, Nathalie  
APPLICANT: BECK, Alain  
TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
FILE REFERENCE: 343 727 - US  
CURRENT APPLICATION NUMBER: US/10/239,313A  
CURRENT FILING DATE: 2002-09-19  
PRIOR APPLICATION NUMBER: FR 00/03711  
PRIOR FILING DATE: 2000-03-23  
PRIOR APPLICATION NUMBER: PCT 01/70772  
PRIOR FILING DATE: 2001-03-22  
NUMBER OF SEQ ID NOS: 697  
SOFTWARE: Patenlin Ver. 2.1  
SEQ ID NO 142  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-239-313A-142

Query Match 87.2%; Score 82; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVPR 15



Db 1 ENPVVHFFKNIVTPR 15

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RESULT 15
US-10-362-264-5
; Sequence 5, Application US/10362264
; Publication No. US20030191063A1
; GENERAL INFORMATION:
; APPLICANT: Wealth, David
; APPLICANT: Anderson, Stephen
; APPLICANT: Mazza, Graziella
; APPLICANT: Ponsford, Mary
; APPLICANT: Streeter, Heather
; APPLICANT: The University of Bristol
; TITLE OF INVENTION: PEPTIDE SELECTION METHOD
; FILE REFERENCE: 1433.004051
; CURRENT APPLICATION NUMBER: US/10/362,264
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/GB01/03702
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 0020618.5
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 0114547.3
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRY
; ORGANISM: Homo sapiens
US-10-362-264-5

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Query Match	87.2%	Score 82;	DB 14;	Length 15;
Best Local Similarity	100.0%	Pred. No. 3.3e-06;		
Matches	15;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
Qy	1	ENPVVHFFKNIVTPR	15	
Db	1	ENPVVHFFKNIVTPR	15	

Search completed: June 7, 2005, 09:50:47  
Job time : 144 secs

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